

## O'Bryen, Barbara

---

**From:** Seharaseyon, Jegatheesan  
**Sent:** Friday, August 30, 2002 11:15 AM  
**To:** O'Bryen, Barbara  
**Subject:** RE: 09/981289  
  
**Importance:** High

Hi,  
Please search SEQ ID NO: 20 of 09/981, 289. Thanks  
J.Seharaseyon  
Art Unit 1647  
CM1 10D16  
10B19 MB  
Phone:(703)-305-1112  
Fax: (703)-746-5177

Point of Contact:  
Barb O'Bryen  
Technical Information Specialist  
STIC CM1 6A05 308-4291

*BoB*  
*9-3-02*

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 30, 2002, 17:23:47 ; Search time 30.33 Seconds

(Without alignments)  
574.962 Million cell updates/sec

Title: US-09-981-289A-20

Perfect score: 804  
Sequence: 1 VRSSRTSPDKPVAHVANP.....RDYLDFAESGVYEGIAL 157

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq.032802:\*

- 1: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA1980.DAT:\*
- 2: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA1981.DAT:\*
- 3: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA1982.DAT:\*
- 4: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA1983.DAT:\*
- 5: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA1984.DAT:\*
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- 7: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA1986.DAT:\*
- 8: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA1987.DAT:\*
- 9: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA1988.DAT:\*
- 10: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA1989.DAT:\*
- 11: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA1990.DAT:\*
- 12: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA1991.DAT:\*
- 13: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA1992.DAT:\*
- 14: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA1993.DAT:\*
- 15: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA1994.DAT:\*
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- 19: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA1998.DAT:\*
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- 21: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA2000.DAT:\*
- 22: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	802	99.8	157	7 AAP60524	Sequence of tumour
2	802	99.8	157	8 AAP70095	Tumour necrosis fa
3	802	99.8	157	8 AAP70144	Amino acid sequenc
4	802	99.8	157	12 AAR14112	Neutrophil stimula
5	802	99.8	157	12 AAR14270	Human TNF. Homo s
6	802	99.8	157	13 AAR27747	Human tumour necro
7	802	99.8	157	14 AAR38069	Human TNF-alpha.
8	802	99.8	157	14 AAR42679	Human tumour Necro
9	802	99.8	157	15 AAR57437	Human tumour necro
10	802	99.8	157	15 AAR60243	Human TNF-alpha.
11	802	99.8	157	15 AAR62463	Tumour necrosis fa

#### ALIGNMENTS

12	802	99.8	157	18 AAW28530	Human TNF. Homo s
13	802	99.8	157	19 AAW40819	Human tumour necro
14	802	99.8	157	20 AAY23242	Human tumour necro
15	802	99.8	157	22 AAG79124	Amino acid sequenc
16	802	99.8	157	22 AAE10848	Human tumour necro
17	802	99.8	157	22 AAG67761	Amino acid sequenc
18	802	99.8	157	22 AAB74783	Wild type human tu
19	802	99.8	158	7 AAP60532	Sequence encoded b
20	802	99.8	158	7 AAP60525	Sequence of tumour
21	802	99.8	158	7 AAP60533	Sequence encoded b
22	802	99.8	158	8 AAP70635	Sequence of tumour
23	802	99.8	158	9 AAP81069	Sequence of new ph
24	802	99.8	158	10 AAP91026	Human tumour necro
25	802	99.8	158	10 AAP93188	Synthetic tumour n
26	802	99.8	158	10 AAP95650	Antitumour peptide
27	802	99.8	158	10 AAP94762	Polypeptide derive
28	802	99.8	158	11 AAR04115	Modified human tum
29	802	99.8	158	11 AAR05613	Antitumour peptide
30	802	99.8	158	11 AAR05807	Polypeptide with a
31	802	99.8	158	11 AAR07901	Human TNF gene pro
32	802	99.8	158	13 AAR20625	Synthetic hTNF. S
33	802	99.8	158	17 AAR88591	Human methionyl-TN
34	802	99.8	158	17 AAR88592	Human methionyl-TN
35	802	99.8	158	22 AAY72933	Human mature tumou
36	802	99.8	159	8 AAP71174	Sequence of human
37	802	99.8	160	9 AAP80161	Biosynthetic multi
38	802	99.8	164	22 AAB82901	Histidine-tagged t
39	802	99.8	180	22 AAY72934	Ompa signal peptid
40	802	99.8	193	19 AAW48246	Tumour necrosis fa
41	802	99.8	193	20 AAW90067	Human TNF-alpha co
42	802	99.8	233	6 AAP50096	Sequence of mature
43	802	99.8	233	7 AAP60555	Sequence of tumour
44	802	99.8	233	7 AAP60531	Sequence of mature
45	802	99.8	233	7 AAP60605	Sequence of tumour

#### RESULT 1

AA60524	standard; Protein: 157 AA.
ID	AA60524
XX	AA60524:
AC	07-AUG-1991 (first entry)
DT	Sequence of tumour necrosis factor (TNF).
XX	Sequence of tumour necrosis factor (TNF).
DE	Anticancer agent; antitumour; antimalarial; tumour necrosis factor.
XX	Anticancer agent; antitumour; antimalarial; tumour necrosis factor.
KW	Anticancer agent; antitumour; antimalarial; tumour necrosis factor.
XX	Anticancer agent; antitumour; antimalarial; tumour necrosis factor.
PN	MO8603751-A.
XX	MO8603751-A.
PD	03-JUL-1986.
XX	03-JUL-1986.
PE	19-DEC-1985; 85MO-EP00721.
XX	19-DEC-1985; 85MO-EP00721.
PR	09-OCT-1985; 85US-0785847.
XX	09-OCT-1985; 85US-0785847.
PR	21-DEC-1984; 84US-0684595.
XX	21-DEC-1984; 84US-0684595.
PR	09-OCT-1986; 86MO-US02133.
XX	09-OCT-1986; 86MO-US02133.
PA	(BIOJ ) BIOGEN NV.
XX	(BIOJ ) BIOGEN NV.
PA	(FIER/) FIERIS W C.
XX	(FIER/) FIERIS W C.
PA	(ALET/) ALLET B.
XX	(ALET/) ALLET B.
PA	(BIOG-) BIOGEN INC.
XX	(BIOG-) BIOGEN INC.
PI	Fiers WC, Fransen LM, Tavernier JHL, Marmenout ALM;
XX	Fiers WC, Fransen LM, Tavernier JHL, Marmenout ALM;
DR	VanDerHeyden J, Allet B, Washima EH;
XX	VanDerHeyden J, Allet B, Washima EH;
DR	WPI: 1986-182891/28.
XX	WPI: 1986-182891/28.
DR	N-PSDB: AAN60442.
XX	N-PSDB: AAN60442.
PT	Mammalian tumour necrosis factors - produced by culturing

PT pro-karyotic hosts transformed with recombinant DNA  
 XX  
 PS Claim 11: Page 66; 93pp; English.

CC TNF-like polypeptides and compsns. are produced by the fermentation  
 CC of host cells transformed with at least one DNA sequence which codes  
 CC for a mammalian TNF-like polypeptide operatively linked to an  
 CC expression control sequence in the transformed host.  
 XX  
 SQ Sequence 157 AA:

Query Match 99.8%; Score 802; DB 7; Length 157;  
 Best Local Similarity 99.4%; Pred. No. 2.2e-75;

Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VRSSSRTPSDKPYAHVAVNPAQAGOLQWLNRRANALLANGVELRDNLVVPSEGLYIYS 60  
 DB 1 vrsssrtpsdckpyahvavnpaagqlqwlrranallangvelrdnqlvvpseglyiys 60

QY 61 QVLFKGGCGPSTHVLTHRTISRAVSQTKVNLISAISKPCQRETPGAEAKPMXEPITL 120  
 DB 61 qvlfkggcgpcsthvllthrtisravsytkvnlisaiskpcqretpgeaakpmxepiyl 120

QY 121 GGVFQLEKGRLSAEINRPYLDPAESGOYFEGITL 157  
 DB 121 ggvflekgrlisaelnrpyldfaesgyvfiglial 157

## RESULT 2

AAP70095  
 ID AAP70095 standard; protein; 157 AA.

AC AAP70095;

DT 04-APR-1991 (first entry)

XX Tumour necrosis factor.

XX Plasmid; tumour necrosis factor; antitumour agent.

XX Escherichia coli.

XX EP220482-A.

PD 06-MAY-1987.

PF 19-SEP-1986; 86EP-0112941.

PR 30-SEP-1985; 85JP-0217740.

XX (SUNR ) SUNTORY LTD.

PI Oshima T, Tanaka S, Matsukura S;

DR WPI; 1987-124161/18.

XX New plasmid for efficient tumour necrosis factor prodn. -  
 PT comprises plasmid with DNA fragment having phage gene derived  
 PT promoter region and E coli derived transcription termination  
 PT sequence

PS Claim 6; page 17-18; 31pp; English.

XX Tumour necrosis factor can be expressed using a plasmid comprising  
 CC a phage gene-derived promoter region upstream of the TNF structural gene  
 CC and an E.coli trp gene terminator joined immediately downstream of a  
 CC base sequence encoding the termination of translation of the structural  
 CC gene. The plasmid is capable of efficient expression of TNF on a large  
 CC scale and with high purity. The transformants may achieve a TNF activity  
 CC 40-300 times as great as with prior transformants. TNF may comprise at  
 CC least 40% of total cell protein. The plasmid lacks a pBR322 derived  
 CC repressor of primer gene. TNF is an antitumour agent.

XX  
 SQ Sequence 157 AA:

Query Match 99.8%; Score 802; DB 8; Length 157;  
 Best Local Similarity 99.4%; Pred. No. 2.2e-75;  
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VRSSSRTPSDKPYAHVAVNPAQAGOLQWLNRRANALLANGVELRDNLVVPSEGLYIYS 60  
 DB 1 vrsssrtpsdckpyahvavnpaagqlqwlrranallangvelrdnqlvvpseglyiys 60

QY 61 QVLFKGGCGPSTHVLTHRTISRAVSQTKVNLISAISKPCQRETPGAEAKPMXEPITL 120  
 DB 61 qvlfkggcgpcsthvllthrtisravsytkvnlisaiskpcqretpgeaakpmxepiyl 120

QY 121 GGVFQLEKGRLSAEINRPYLDPAESGOYFEGITL 157  
 DB 121 ggvflekgrlisaelnrpyldfaesgyvfiglial 157

## RESULT 3

AAP70144  
 ID AAP70144 standard; protein; 157 AA.

AC AAP70144;

DT 13-MAY-1991 (first entry)

XX Amino acid sequence of mature tumour necrosis factor (TNF).

XX Tumour necrosis factor analogue; lymphokine; anti-tumour.

XX EP220966-A.

PD 06-MAY-1987.

PF 30-OCT-1986; 86EP-0308484.

PR 22-MAY-1986; 86US-0866213.

PR 30-OCT-1985; 85US-0792815.

XX (CETU ) CETUS CORP.

PI Iain LSL, Dorin G, Yamamoto R, Hanisch WH, Thomson JW;

PI Wolfe SN.

XX WPI; 1987-124486/18.

DR Purified recombinant tumour necrosis factor compsn. - obt'd. by

PT using a hydrophobic matrix to retain the factor followed by

PT chromatographic elution

PS Disclosure; Fig 3; 25pp; English.

XX Specific examples of TNF analogues include N-terminally deleted  
 CC species of the protein, including those having deletions of the  
 CC N-terminal 1,2,3,4,5,6,7,8,9,10,14, and 31 AA's of the SQ in AAP70144.  
 CC Mutelins lacking up to and including the first ten AA's at the  
 CC N-terminus have been found to have comparable or greater specific  
 CC activities as compared to the TNF of the SQ shown in AAP70144. Other  
 CC mutelins of TNF covered by the method of the invention include  
 CC species of TNF in which any or all of the cysteine residues have  
 CC been converted to serine or other neutral AA's for example, glycine  
 CC or alanine. In general, neutral AA replacements of the cysteine at  
 CC position 69 result in active TNF proteins. It appears that the  
 CC cysteine at position 101 is also dispensable.

XX Sequence 157 AA:

Query Match 99.8%; Score 802; DB 8; Length 157;  
 Best Local Similarity 99.4%; Pred. No. 2.2e-75;

Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VRSSRTPSDKPAHVAVNPQAEGLQWLNRRANALLANGVELRDNLVPSGLYLTVS 60  
 DB 1 VRSSRTPSDKPAHVAVNPQAEGLQWLNRRANALLANGVELRDNLVPSGLYLTVS 60  
 QY 61 QVLEKGGCPSSTHVLHTTISRIVSYOTKYNLSAISKPCQRETPEGAEAKPMXEPYTL 120  
 DB 61 QVLEKGGCPSSTHVLHTTISRIVSYOTKYNLSAISKPCQRETPEGAEAKPMXEPYTL 120  
 QY 121 GGVFQLEKGRDLAEINRPDYLDFAESGOVYFGIATL 157  
 DB 121 GGVFQLEKGRDLAEINRPDYLDFAESGOVYFGIATL 157

RESULT 4  
 AAR14112  
 ID AAR14112 standard; peptide: 157 AA.  
 AC AAR14112;  
 XX 11-DEC-1991 (first entry)  
 DE Neutrophil stimulating peptide.  
 XX hTNF; AIDS; cancer; inflammatory syndromes; rheumatoid arthritis;  
 KM adult respiratory distress syndrome; human tumour necrosis factor.  
 XX synthetic.  
 OS

Key Location/Qualifiers  
 FH 111..120  
 FT /label= peptide 275  
 FT 1..18  
 FT /label= peptide 301  
 FT 43..58  
 FT /label= peptide 302  
 FT 94..109  
 FT /label= peptide 303  
 FT 63..83  
 FT /label= peptide 304  
 FT /note= "neutrophil stimulating activity"  
 FT 132..150  
 FT /label= peptide 305  
 FT 13..26  
 FT /label= peptide 306  
 FT 22..40  
 FT /label= peptide 307  
 FT 54..68  
 FT /label= peptide 308  
 FT /note= "neutrophil stimulating activity and selective effects on neutrophil degranulation"  
 FT 73..94  
 FT /label= peptide 309  
 FT /note= "neutrophil stimulating activity"  
 FT 79..89  
 FT /label= peptide 323  
 FT 76..84  
 FT /label= peptide 393  
 FT 81..94  
 FT /label= peptide 394  
 FT 70..80  
 FT /label= peptide 395  
 FT /note= "neutrophil stimulating activity"  
 FT 84..94  
 FT /label= peptide 396  
 XX  
 PN W09113908-A.  
 XX  
 XX 19-SEP-1991.  
 PD  
 XX 12-MAR-1991; 91WO-AU00086.

XX 12-MAR-1990; 90AU-0009065.  
 PR  
 XX (PEPT-) PEPTIDE TECHN LTD.  
 PA  
 XX Rathjen DA, Ferrante A;  
 PI  
 XX WPI: 1991-295580/40.  
 DR  
 XX New neutrophil stimulating peptide(s) derived from human TNF -  
 FT useful for treating depressed neutrophil function in e.g. AIDS  
 FT and cancer, and inflammatory syndrome in e.g. rheumatoid  
 PT arthritis  
 PS  
 XX Disclosure; Fig 1; 27pp: English.  
 XX The amino acid sequence codes for human tumour necrosis factor.  
 CC Peptides derived from this sequence have neutrophil stimulating  
 CC activity. The peptides were synthesised using the Fmoc-polyamide  
 CC method of solid peptide synthesis. Treatment with the peptides  
 CC can be used to restore depressed or aberrant neutrophil activity  
 CC without causing the side effects associated with the therapeutic  
 CC use of the whole TNF molecule. Such peptides can be used in the  
 CC treatment of individuals suffering from AIDS, cancer or  
 CC inflammatory syndromes e.g. rheumatoid arthritis or adult  
 CC respiratory distress syndrome.  
 XX  
 SQ Sequence 157 AA:

Query Match 99.8%; Score 802; DB 12; Length 157;  
 Best Local Similarity 99.4%; Pred. No. 2.2e-75;  
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VRSSRTPSDKPAHVAVNPQAEGLQWLNRRANALLANGVELRDNLVPSGLYLTVS 60  
 DB 1 VRSSRTPSDKPAHVAVNPQAEGLQWLNRRANALLANGVELRDNLVPSGLYLTVS 60  
 QY 61 QVLEKGGCPSSTHVLHTTISRIVSYOTKYNLSAISKPCQRETPEGAEAKPMXEPYTL 120  
 DB 61 QVLEKGGCPSSTHVLHTTISRIVSYOTKYNLSAISKPCQRETPEGAEAKPMXEPYTL 120  
 QY 121 GGVFQLEKGRDLAEINRPDYLDFAESGOVYFGIATL 157  
 DB 121 GGVFQLEKGRDLAEINRPDYLDFAESGOVYFGIATL 157

RESULT 5  
 AAR14270  
 ID AAR14270 standard; peptide: 157 AA.  
 AC AAR14270;  
 XX 09-JAN-1992 (first entry)  
 DE Human TNF.  
 XX  
 XX Tumour necrosis factor; cytotoxic; metastasis.  
 KW  
 XX Homo sapiens.  
 OS  
 XX

Key Location/Qualifiers  
 FH 111..120  
 FT /label= #275  
 FT 1..18  
 FT /label= #301  
 FT 43..58  
 FT /label= #302  
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 FT 94..109  
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 FT 63..83  
 FT /label= #304

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FT	Peptide	22..40	
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FT	/note=	claim 3 "	
FT	Peptide	73..94	
FT	/label=	#309	
FT	/note=	claim 5 "	
FT	Peptide	79..89	
FT	/label=	#323	
FT	Peptide	81..94	
FT	/note=	claim 6 "	
FT	Peptide	70..80	
FT	/note=	claim 7 "	
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PN	WO9114702-A.		
XX			
PD	03-OCT-1991.		
XX			
PE	15-MAR-1991;	91WO-AU00100.	
XX			
PR	22-NOV-1990;	90AU-0003477.	
PR	19-MAR-1990;	90AU-0009156.	
XX			
PA	(PEPT-) PEPTIDE TECHN LTD.		
XX			
PI	Rachjen D, Aston R;		
XX			
DR	WPI; 1991-310534/42.		
XX			
PT	New cytotoxic and/or proliferation-inhibiting polypeptide		
PT	fragments - useful in treatment of tumours with reduced side		
PT	effects.		
XX			
PS	Claim 1; Fig 1; 35pp; English.		
XX			
CC	The peptide fragments indicated in the feature table have cytotoxic		
CC	and/or inhibition of proliferation effects on tumour cells. The		
CC	peptides may be co-administered with whole TNF alpha or with a		
CC	cyto-toxic drug.		
XX			
SQ	Sequence 157 AA;		
	Query Match	99.8%; Score 802; DB 12; Length 157;	
	Best Local Similarity	99.4%; Pred. No. 2,2e-75;	
	Matches 156; Conservative	0; Mismatches 1; Indels 0; Gaps	0.
OY	1 VRSSRTPSDKPVAVVAVNPQAEGQLQWLMRRANMLLANGVELRDNLQVVPSEGLYLIYS	60	
DB	1 VRSSRTPSDKPVAVVAVNPQAEGQLQWLMRRANMLLANGVELRDNLQVVPSEGLYLIYS	60	
OY	61 QVLEFGGQGPSTHVLLTHTISRIAVSYQTKVNLSSAIKSPCOREPPEGAEAKPWKEPIYL	120	
DB	61 QVLEFGGQGPSTHVLLTHTISRIAVSYQTKVNLSSAIKSPCOREPPEGAEAKPWKEPIYL	120	
OY	121 GGVFQLEKGDRLSAETINRPDYLDPAESGGVYFGIALL	157	
DB	121 GGVFQLEKGDRLSAETINRPDYLDPAESGGVYFGIALL	157	
RESULT	6		
ID	AAR27747		
XX	AAR27747 standard; protein; 157 AA.		
AC	AAR27747;		
DT	03-MAR-1993 (first entry)		

XX	Human tumour necrosis factor alpha.
DE	
XX	hTNF; monoclonal antibody; sepsis syndrome, cachexia, microbial;
KW	infection; rheumatoid arthritis; inflammation.
KW	
OS	Homo sapiens.
XX	
XX	
FT	Key
FT	Location/Qualifiers
FT	1..20
FT	/note= "putative receptor binding portion"
FT	11..13
FT	/note= "putative receptor binding portion"
FT	37..42
FT	/note= "putative receptor binding portion"
FT	49..57
FT	/note= "putative receptor binding portion"
FT	155..157
FT	/note= "putative receptor binding portion"
FT	59..80
FT	/note= "epitope for Ab binding"
FT	87..108
FT	/note= "epitope for Ab binding"
XX	
XX	W09216553-A.
XX	
XX	01-OCT-1992.
XX	
XX	18-MAR-1992; 92WO-US02190.
XX	
XX	18-MAR-1991; 91US-0670827.
XX	
XX	(CENZ ) CENTOCOR INC.
XX	
XX	Daddona PE, Ghraieb J, Knight DM, Le J, Siegel SA;
XX	Vilcek J;
XX	
XX	WPI: 1992-349155/42.
XX	
XX	Monoclonal and chimeric antibodies to human TNF - useful for
XX	treating sepsis syndrome, cachexia, microbial infections,
XX	rheumatoid arthritis, inflammation, etc.
XX	
XX	Claim 22; Page 77; 105pp; English.
XX	
XX	Anti-TNF antibodies were prepd. which bound to an epitope of at
XX	least 5 amino acids of residues 87-108 or both of residues 59-80 and
XX	87-108 of human tumour necrosis factor alpha, but do not bind known
XX	or putative receptor binding portions of TNF, such as those shown in
XX	the features table. The antibodies may be prepd. by hybridomas or
XX	recombinantly and may be used for in vivo treatment and diagnosis of
XX	human pathologies associated with TNF e.g. sepsis syndrome, cachexia,
XX	circulatory collapse and shock resulting from acute or chronic
XX	bacterial infection, acute and parasitic or infectious processes,
XX	including bacterial, viral and fungal infections, acute and chronic
XX	immune and autoimmune pathologies such as sarcoioidosis and Crohn's
XX	disease, vascular inflammatory pathologies such as disseminated
XX	intravascular coagulation, graft vs. host disease, Kawasaki's disease
XX	and malignant tumours. The antibodies may be used in combination with
XX	TNF therapy, e.g. cancer therapy to remove the undesired side effects.
XX	They may also be used to remove TNF from fluids, tissues or cells, to
XX	detect or quantitate TNF and for blocking TNF activity in vivo, in
XX	situ and in vitro.
XX	
XX	Sequence 157 AA;
XX	
XX	Query Match 99.8%; Score 802; DB 13; Length 157;
XX	Best Local Similarity 99.4%; Pred. No. 2,2e-75;
XX	Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Db      1  vrsssrtpsdkpyahvvanpqaegqlqwlntrranallangvelrdnqlvvpseglyliys 60
QY      61  QVLFKGGCGPSTHVLLTHRTSRIVASYQTKVNLISAIKSPCORETEPGAAKPKWPEPIYL 120
Db      61  qvlfkqgpcsthvllthrtslrivasqtkvnlisaikspcqretpegaaekpwpepiyl 120
QY      121  GGVFQLEKGDRLSAEINRPDYLDFAESGQYFGIIAL 157
Db      121  ggvfqlkekqdrisaelnrpdyldfaesgvyfgliial 157

RESULT  7
AAR38069
ID      AAR38069 standard; protein; 157 AA.
XX
AC      AAR38069;
XX
DT      14-OCT-1993 (first entry)
XX
DE      Human TNF-alpha.
XX
KW      Withdrawal symptom; tumour necrosis factor; narcotic; nicotine;
        morphine; thymosin; alcohol.
XX
OS      Homo sapiens.
XX
PN      JP05117161-A.
XX
PD      14-MAY-1993.
XX
PF      23-OCT-1991; 91JP-0337489.
XX
PR      23-OCT-1991; 91JP-0337489.
XX
PA      (MIZU/) MIZUNO D.
XX
PS      (SOMA/) SOMA G.
XX
DR      WPI; 1993-191442/24.
XX
PT      Drugs for treating alcohol, morphine narcotics or nicotine
        withdrawal symptoms - contg. tumour necrosis factor-alpha,
        thymosin tumour necrosis factor fused cpd. or murine tumour
        necrosis factor-alpha prepd. from macrophage of human or animal
XX
PS      Disclosure; Page 2-3; 5pp; Japanese.
XX
CC      Drugs acting on withdrawal symptoms contain TNF, esp. TNF-alpha
        (AAR38069 and AAR38077), rTNF-S-AM1 (AAR38070), rTNF-S-AM2 (AAR38071),
        thymosin-beta4-TNF fused cpd. (AAR38072-76).
XX
CC      The drugs are effective in treatment of withdrawal symptoms caused
        by habitual use of alcohol, morphine narcotics or nicotine in humans
        or animals (e.g. swine, dog, cat, chicken). The drugs may be
        administered as TNF at a dose of 10ng-10mg orally or 5ng-1mg i.v.
        or 50ng-50mg percutaneously a day for a human adult. In animals,
        CC the drugs may be administered according to the human dosage (1/60
        per kg body wt.).
XX
SQ      Sequence 157 AA:

Query Match          99.8%; Score 802; DB 14; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.2e-75;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1  VRSSSRTPSDKPYAHVVANPQAEQQLQWLNRANALLANGVELRDNQLVVPSEGLYLIYS 60
Db      1  vrsssrtpsdkpyahvvanpqaegqlqwlntrranallangvelrdnqlvvpseglyliys 60
QY      61  QVLFKGGCGPSTHVLLTHRTSRIVASYQTKVNLISAIKSPCORETEPGAAKPKWPEPIYL 120
Db      61  qvlfkqgpcsthvllthrtslrivasqtkvnlisaikspcqretpegaaekpwpepiyl 120
QY      121  GGVFQLEKGDRLSAEINRPDYLDFAESGQYFGIIAL 157
Db      121  ggvfqlkekqdrisaelnrpdyldfaesgvyfgliial 157

```

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Db      121  ggvfqlkekqdrisaelnrpdyldfaesgvyfgliial 157

RESULT  8
AAR42679
ID      AAR42679 standard; Protein; 157 AA.
XX
AC      AAR42679;
XX
DT      19-APR-1994 (first entry)
XX
DE      Human Tumour Necrosis Factor alpha.
XX
KW      plasmid pDS56/RBSII, Sphi-TNF-alpha; mutein; inflammation; obesity;
        septic shock; treatment; mutagenic PCR; cytokine.
XX
OS      Homo sapiens.
XX
PN      EP563714-A.
XX
PD      06-OCT-1993.
XX
PF      20-MAR-1993; 93EP-0104591.
XX
PR      02-APR-1992; 92EP-0810249.
XX
PA      (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI      Lesslauer W, Lotscher H, Stuber D, Loetscher H;
        Stueber D;
XX
DR      WPI; 1993-313109/40.
XX
DR      N-PSDB; AAQ49223.
XX
PT      New human Tumour Necrosis Factor mutein(s) - have amino acid
        change at position 86, for selective binding affinity to the
        p55-TNF-Receptor
XX
PS      Disclosure; Fig 1b; 29pp; English.
XX
CC      The human TNF-alpha expression plasmid pDS56/RBSII, Sphi-TNF-alpha
        was used as the source of TNF-alpha gene for preparing the various
        CC TNF-alpha mutants of the invention. Mutagenic PCR was used on the
        CC wild-type template to introduce amino acid substitutions at sites
        CC affecting binding specificity. The mutants retain binding activity
        CC to the human p55-TNF-Receptor but do not bind to the human p75-TNF-
        CC Receptor. Consequently, the mutants have lower systemic
        CC toxicity and only elicit some of the activities of wild-type TNF-a.
XX
SQ      Sequence 157 AA:

Query Match          99.8%; Score 802; DB 14; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.2e-75;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1  VRSSSRTPSDKPYAHVVANPQAEQQLQWLNRANALLANGVELRDNQLVVPSEGLYLIYS 60
Db      1  vrsssrtpsdkpyahvvanpqaegqlqwlntrranallangvelrdnqlvvpseglyliys 60
QY      61  QVLFKGGCGPSTHVLLTHRTSRIVASYQTKVNLISAIKSPCORETEPGAAKPKWPEPIYL 120
Db      61  qvlfkqgpcsthvllthrtslrivasqtkvnlisaikspcqretpegaaekpwpepiyl 120
QY      121  GGVFQLEKGDRLSAEINRPDYLDFAESGQYFGIIAL 157
Db      121  ggvfqlkekqdrisaelnrpdyldfaesgvyfgliial 157

RESULT  9
AAR57437
ID      AAR57437 standard; protein; 157 AA.

```

XX AAR57437;  
 AC 13-MAR-1995 (first entry)  
 DE Human tumour necrosis factor (wild-type).  
 XX  
 XX Tumour necrosis factor; TNF; mutein; variant; antitumour;  
 KW toxicity; haemorrhagic necrosis; antiviral; parasite; malaria.  
 XX Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 1..7 "One or more of the first 7 N-terminal  
 FT /note= amino acids may be deleted"  
 FT Misc-difference 4 /note= "Ser pref. replaced by Arg"  
 FT Misc-difference 5 /note= "Ser pref. replaced by Arg"  
 FT Misc-difference 6 /note= "Arg pref. replaced by Ala"  
 FT Misc-difference 7 /note= "Thr pref. replaced by His or Lys"  
 FT Misc-difference 8 /note= "Pro pref. replaced by Arg"  
 FT Misc-difference 9 /note= "Ser pref. replaced by Lys"  
 FT Misc-difference 10 /note= "Asp pref. replaced by Arg"  
 FT Misc-difference 38 /note= "Ala pref. replaced by Asp"  
 FT Misc-difference 39 /note= "Asn pref. replaced by Asp, Lys or Val"  
 FT Misc-difference 40 /note= "Gly pref. replaced by Asp, Lys or Val"  
 FT Misc-difference 41 /note= "Val pref. replaced by Ser"  
 FT Misc-difference 52 /note= "Ser pref. replaced by Ile, Glu or Lys"  
 FT Misc-difference 53 /note= "Glu pref. replaced by Lys or Leu"  
 FT Misc-difference 54 /note= "Gly pref. replaced by Asp or Val"  
 FT Misc-difference 56 /note= "Tyr pref. replaced by Phe or Glu"  
 FT Misc-difference 85 /note= "Val pref. replaced by Glu or Arg"  
 FT Misc-difference 86 /note= "Ser pref. replaced by Leu, Lys, Glu or Asp"  
 FT Misc-difference 87 /note= "Tyr pref. replaced by Glu or Arg"  
 FT Misc-difference 88 /note= "Gln pref. replaced by Glu"  
 FT Misc-difference 127 /note= "Glu pref. replaced by Ala, Val or Lys"  
 FT Misc-difference 128 /note= "Lys pref. replaced by Ala, Val or Glu"  
 FT Misc-difference 129 /note= "Gly pref. replaced by Glu, Lys or Val"  
 FT Misc-difference 156 /note= "Ala pref. replaced by Asp"  
 FT Misc-difference 157 /note= "Leu pref. replaced by Phe"  
 FT  
 XX DE4404124-A.  
 XX 11-AUG-1994.  
 XX 09-FEB-1994; 94DE-4404124.  
 XX 09-FEB-1993; 93KR-0001751.

PA (HANI-) HANIL SYNTHETIC FIBER CO LTD.  
 XX Kang S, Lee I, Shin H-C, Shin N-K;  
 XX WPI; 1994-250457/31.  
 DR N-PSDB; AAO67089.  
 XX  
 XX New tumour necrosis factor muteins and related DNA - also vectors  
 PT and transformed cells, with increased antitumour activity and  
 PT lower toxicity than wild type protein  
 XX  
 XX Claim 1; Page 20; 23pp; German.  
 PS  
 XX  
 CC TNF muteins are claimed, in which at least one amino acid at  
 CC positions 4-10, 38-41, 52-54, 56, 85-88, 127-129, 156 or 157 is  
 CC exchanged for a different amino acid. Opt. one or more of the first  
 CC 7 N-terminal amino acids is deleted. TNF causes haemorrhagic  
 CC necrosis of tumours; has anti-viral activity and inactivates some  
 CC species of malarial parasites. The muteins have increased antitumour  
 CC activity and lower toxicity than wild-type protein.  
 XX  
 SQ Sequence 157 AA:  
 Query Match 99.8%; Score 802; DB 15; Length 157;  
 Best Local Similarity 99.4%; Pred. No. 2.2e-75;  
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 VRSSRTSPDKPYAHVYVAMPQAEGLQWLNRRANALLANGVELRDQLYVPSGLYIYS 60  
 DB 1 VRSSRTSPDKPYAHVYVAMPQAEGLQWLNRRANALLANGVELRDQLYVPSGLYIYS 60  
 QY 61 QVLFKQCGCPSTHVLTHTRISRIAVSYQTRKVNLSAIKSPCQRETPEGAEANFPMXEPYIL 120  
 DB 61 QVLFKQCGCPSTHVLTHTRISRIAVSYQTRKVNLSAIKSPCQRETPEGAEANFPMXEPYIL 120  
 QY 121 GGVFQLEKGDRLSAETINRPDYLDFAESGOVYRGITIL 157  
 DB 121 GGVFQLEKGDRLSAETINRPDYLDFAESGOVYRGITIL 157  
 RESULT 10  
 AAR60243  
 ID AAR60243 standard; peptide; 157 AA.  
 XX  
 AC AAR60243;  
 XX  
 DT 16-MAR-1995 (first entry)  
 XX  
 DE Human TNF-alpha.  
 XX  
 XX TNF-alpha; tumor necrosis factor-alpha; tip peptide; mutein; cancer;  
 KW sepsis; inflammation; cytokine; metastasis; lectin; adhesion;  
 KW mutagenesis.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 1..8 "in TNF muteins, residues 1-8 are replaced  
 FT /note= by a peptide within the region spanning  
 FT aa 5-30 of laminin"  
 FT Misc-difference 101 /note= "in TNF muteins, residue 101 is Ser"  
 FT Misc-difference 102 /note= "in TNF muteins, residue 102 is Arg or  
 FT deleted"  
 FT Misc-difference 103 /note= "in TNF muteins, residue 103 is Trp"  
 FT Misc-difference 105 /note= "in TNF muteins, residue 105 is Pro or Ile  
 FT or residue 105 is Ile and residue 44 is Cys"  
 FT Misc-difference 106



```
FT /note- "In TNF muteins, residue 106 is Ser, or
FT MISC-difference 108 residue 106 is Ser and residue 131 is Cys"
FT MISC-difference 110 /note- "In TNF muteins, residue 108 is Phe"
FT MISC-difference 110 /note- "In TNF muteins, residue 110 is Lys"
FT MISC-difference 111.112 /note- "In TNF muteins, residues 111-112 are
FT deleted, or residue 111 is deleted
FT or Met, or residue 109 is Gln and residue 120 is His"
FT MISC-difference 115 /note- "In TNF muteins, residue 115 is Ile or Cys"
FT MISC-difference 116 /note- "In TNF muteins, residue 116 is Lys, His or
FT Val"
FT MISC-difference 115.116 /note- "In TNF muteins, residues 115-116 are
FT Ile-Lys"
FT MISC-difference 115.116 /note- "In TNF muteins, residues 115-116 are
FT Ile-Lys"
PN WO9418325-A.
PD 18-AUG-1994.
PF 02-FEB-1994; 94WO-EP00286.
PR 03-FEB-1993; 93EP-0400262.
PA (INNO-) INNOGENETICS NV SA.
PI De Baetselier P, Franssen L, Lucas R, Sablon E;
PI WPI; 1994-279746/34.
DR New tumour necrosis factor -alpha muteins, antibodies and
XX antitense peptide(s) - used in the treatment of diseases and
XX PT conditions associated with the in vivo activities of TNF-A eg
XX cancer, sepsis, inflammation, etc
XX PS Disclosure; Page 10; 132pp; English.
XX CC TNF-alpha muteins were constructed in the tip region (given in
XX CC AAR602463) of human TNF-alpha. The mutations resulted in:
XX CC modulation of lectin-like activity; reduced toxic activity;
XX CC modulation of inflammatory activity; modulated adhesion molecule
XX CC increasing capacity; reduced metastasis promoting activity; and/or
XX CC increased half-life. Muteins of the mouse TNF (given in AAR60244)
XX CC may also be produced.
XX CC
XX SQ Sequence 157 AA;
Query Match 99.8%; Score 802; DB 15; Length 157;
Best Local Similarity 99.4%; Pred. NO. 2.2e-75;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 VRSSSRTPSDKPVAVHVNPAQEGOLWLNRRANLLANGVELRDNOI.VVSEGLIYLS 60
DB 1 VRSSSRTPSDKPVAVHVNPAQEGQLQWLNRRANLLANGVELRDNOI.VVSEGLIYLS 60
OY 61 QVLEFKGQGCPSSTHVLITHTISRIASVYQTKVNL.SAIKSPCOREPPEGAEAKPMXEPITL 120
DB 61 QVLEFKGQGCPSSTHVLITHTISRIASVYQTKVNL.SAIKSPCOREPPEGAEAKPMXEPITL 120
OY 121 GGVFQLEKGRDLSAIFNRPDYLDFAESQVYFGIITL 157
DB 121 GGVFQLEKGRDLSAIFNRPDYLDFAESQVYFGIITL 157
RESULT 11
AAR62463
ID AAR62463 standard; Protein; 157 AA.
XX
```

```
AC AAR62463;
XX 02-JUN-1995 (first entry)
DT Tumour necrosis factor-alpha protein.
DE Human; tumour necrosis factor; TNF; TNF-a; expression; mutein; mutation;
KW receptor; affinity; therapeutic; diagnostic; cancer therapy; cancer;
XX obesity; septic shock; meningitis.
OS Homo sapiens.
XX EP619372-A.
XX 12-OCT-1994.
XX 17-MAR-1994; 94EP-0104154.
XX 29-MAR-1993; 93EP-0810224.
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX Banner D, Lesslauer W, Lotscher H, Stuber D, Loetscher H;
XX Stueber, D;
XX WPI; 1994-311810/39.
XX N-PSDB; AAQ73431.
XX New human TNF-a muteins with higher affinity for p75-TNFR -
XX useful e.g. for cancer therapy, treatment of obesity and toxic
XX shock
XX PS Disclosure; Page 28-31; 53pp; English.
XX CC The amino acid sequence of the human wild type tumour necrosis factor
XX CC alpha (TNF-a). The gene encoding the protein is placed in the expression
XX CC plasmid pDS56/RBSII and called pDS56/RBSII.SphI-TNFR. The expression of
XX CC the wild type or mutein proteins is regulated by the lac repressor
XX CC present on the plasmid prep4. The gene encoding the protein is mutated
XX CC at specific sites resulting in series of mutated proteins (AAR62464-83
XX CC and AAR63093-103). The biological activities of TNF are mediated via
XX CC specific receptors of mol. wt. 55 and 75 kDa called p55-TNF-R and
XX CC p75-TNF-R respectively. The mutated protein presented have a higher
XX CC affinity for the human p75-TNF receptor than for the p55-TNF receptor.
XX CC The mutated proteins can be used in a variety of therapeutic or
XX CC diagnostic applications including cancer therapy, treatment of obesity,
XX CC septic shock or bacterial meningitis.
XX CC
XX SQ Sequence 157 AA;
Query Match 99.8%; Score 802; DB 15; Length 157;
Best Local Similarity 99.4%; Pred. NO. 2.2e-75;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 VRSSSRTPSDKPVAVHVNPAQEGOLWLNRRANLLANGVELRDNOI.VVSEGLIYLS 60
DB 1 VRSSSRTPSDKPVAVHVNPAQEGQLQWLNRRANLLANGVELRDNOI.VVSEGLIYLS 60
OY 61 QVLEFKGQGCPSSTHVLITHTISRIASVYQTKVNL.SAIKSPCOREPPEGAEAKPMXEPITL 120
DB 61 QVLEFKGQGCPSSTHVLITHTISRIASVYQTKVNL.SAIKSPCOREPPEGAEAKPMXEPITL 120
OY 121 GGVFQLEKGRDLSAIFNRPDYLDFAESQVYFGIITL 157
DB 121 GGVFQLEKGRDLSAIFNRPDYLDFAESQVYFGIITL 157
RESULT 12
AAW28530
ID AAW28530 standard; Protein; 157 AA.
XX AAW28530;
XX
```

[illegible][illegible]



XX (CENZ ) CENTOCOR INC.  
 PA  
 XX  
 PI Le J, Vilecek J, Daddona P, Ghayeb J, Knight D, Siegel S;  
 XX  
 DR WPI; 2001-615872/71.  
 XX  
 PT New chimeric antibody binding an epitope specific for human tumour  
 PT necrosis factor alpha useful in treatment and diagnosis of tumour  
 PT necrosis factor alpha related conditions e.g. Crohn's disease  
 XX  
 PS Disclosure; Fig 13; 93pp; English.  
 XX  
 CC The present sequence represents human tumour necrosis factor  
 CC (TNF)-alpha. The specification describes a chimeric antibody which  
 CC binds an epitope specific for human TNF-alpha. The antibody comprises  
 CC at least part of a human immunoglobulin constant region and at least  
 CC part of a non-human immunoglobulin variable region. The chimeric  
 CC antibodies are useful in vivo diagnosis and therapy of TNF-alpha-  
 CC mediated pathologies and conditions. They can also neutralize human  
 CC TNF-alpha under physiological conditions. This is useful as TNF is  
 CC known to be involved in e.g. pro-inflammatory actions, wasting  
 CC associated with cancer and other diseases (cachexia), gram-negative  
 CC sepsis and endotoxemic shock. Antibodies can be used to treat and/or  
 CC diagnose bacterial, parasitic or viral infections, chronic inflammatory  
 CC diseases, auto-immune diseases, malignancies and neurodegenerative  
 CC diseases (such as Crohn's disease and Rheumatoid arthritis). As  
 CC inhibition or antagonism of TNF also decreases the expression of  
 CC vascular endothelial growth factor (VEGF), the antibodies are also  
 CC useful to treat VEGF-mediated diseases.  
 XX  
 SQ Sequence 157 AA;

Query Match 99.8%; Score 802; DB 22; Length 157;  
 Best Local Similarity 99.4%; Pred. No. 2.2e-75;  
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VRSSSRTPSDKPVAVHVPANPOAEQLOMINRRANALLANGVELRDNQLVPSSEGLYLIYS 60  
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 Db 1 VRSSSRTPSDKPVAVHVPANPOAEQQLWLNRRANALLANGVELRDNQLVPSSEGLYLIYS 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 61 QVLFKGGCGPSTHVLHTTISRIVSYQTKVNLSAIKSPCORETPGAEAKPWXPPIYL 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 qvlfkgqgcpsthlhttsrriavsyqtkvnlssaikspcoretpgaaekpwypelyl 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 121 GGVFQLEKGRLSAELNRPDYLDFAESGQVYFGIALL 157  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 ggvfqlkxgdrisaelnrdpyldfaesgvyfgyfiall 157

Search completed: August 30, 2002, 17:36:15  
 Job time: 748 sec

GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: August 30, 2002, 17:26:07 ; Search time 13.09 Seconds

(without alignments)  
292.938 Million cell updates/sec

Title: US-09-981-289A-20

Perfect score: 804  
Sequence: 1 VRSSRRTPSDKPAHVAVNP.....RPDYDFAESGQVYGIATL 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Issued\_Patents\_AA:\*  
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2: /cgn2\_6/prodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	802	99.8	157	1	US-07-794-400-1
2	802	99.8	157	1	US-08-041-648-2
3	802	99.8	157	1	US-08-107-235-1
4	802	99.8	157	1	US-08-217-529-2
5	802	99.8	157	1	US-08-318-193-86
6	802	99.8	157	1	US-08-397-470-1
7	802	99.8	157	1	US-08-192-102-1
8	802	99.8	157	1	US-08-324-799-1
9	802	99.8	157	1	US-08-538-875-1
10	802	99.8	157	2	US-08-394-600B-17
11	802	99.8	157	2	US-08-500-860A-35
12	802	99.8	157	2	US-08-192-861A-1
13	802	99.8	157	2	US-08-600-783-5
14	802	99.8	157	3	US-08-584-031-13
15	802	99.8	157	3	US-08-714-960B-1
16	802	99.8	157	4	US-09-133-119-1
17	802	99.8	157	4	US-08-192-093A-1
18	802	99.8	157	5	PCT-US92-02190-1
19	802	99.8	157	5	PCT-US93-02475-1
20	802	99.8	157	5	PCT-US95-02513-17
21	802	99.8	157	6	5180811-1
22	802	99.8	177	2	US-08-394-600B-21
23	802	99.8	177	5	PCT-US95-02513-21
24	802	99.8	153	2	US-08-889-909A-3
25	802	99.8	153	4	US-09-156-163A-3
26	802	99.8	233	1	US-08-323-445A-10
27	802	99.8	233	1	US-08-515-903A-10

28	802	99.8	233	2	US-08-912-227-3	Sequence 3, Appl1
29	802	99.8	233	2	US-08-230-428B-2	Sequence 2, Appl1
30	802	99.8	233	4	US-08-883-086-6	Sequence 6, Appl1
31	802	99.8	233	4	US-08-880-342-37	Sequence 37, Appl1
32	802	99.8	233	5	PCT-US95-12840-10	Sequence 10, Appl1
33	802	99.8	233	6	5422425-2	Patent No. 5422425
34	800	99.5	157	1	US-07-940-605A-5	Sequence 5, Appl1
35	800	99.5	157	2	US-08-690-096-5	Sequence 5, Appl1
36	799	99.4	158	6	5182196-2	Patent No. 5182196
37	798	99.3	156	1	US-08-323-445A-19	Sequence 19, Appl1
38	797	99.1	158	1	US-07-794-400-6	Sequence 6, Appl1
39	797	99.1	158	1	US-07-794-400-7	Sequence 7, Appl1
40	797	99.1	158	1	US-07-794-400-8	Sequence 8, Appl1
41	797	99.1	158	1	US-08-397-470-6	Sequence 6, Appl1
42	797	99.1	158	1	US-08-397-470-7	Sequence 7, Appl1
43	797	99.1	158	1	US-08-387-470-8	Sequence 8, Appl1
44	796	99.0	158	1	US-07-794-400-4	Sequence 4, Appl1
45	796	99.0	158	1	US-08-397-470-4	Sequence 4, Appl1

## ALIGNMENTS

RESULT 1  
US-07-794-400-1  
: Sequence 1, Application US/077944400  
: Patent No. 5422104  
: GENERAL INFORMATION:  
: APPLICANT: Fiers, W.  
: APPLICANT: Tavernier, J.  
: APPLICANT: Van Oostede, X.  
: TITLE OF INVENTION: TNF-Mutlins  
: NUMBER OF SEQUENCES: 24  
: CORRESPONDENCE ADDRESSES:  
: ADDRESSEE: Hoffmann-La Roche Inc.  
: STREET: 340 Kingsland Street  
: CITY: Nutley  
: STATE: New Jersey  
: COUNTRY: USA  
: ZIP: 07110  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patentin Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/07/794,400  
: FILING DATE: 19911120  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: EP 90810901.0  
: FILING DATE: 21-NOV-1990  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Krovatin, William  
: REGISTRATION NUMBER: 33256  
: REFERENCE/DOCKET NUMBER: 4105/136-00  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (201) 235-4387  
: TELEFAX: (201) 235-3500  
: INFORMATION FOR SEQ ID NO: 1:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 157 amino acids  
: TYPE: AMINO ACID  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
: ORIGINAL SOURCE:  
: ORGANISM: Homo sapiens  
: TISSUE TYPE: Blood  
: CELL TYPE: Macrophage  
: US-07-794-400-1

Query Match 99.8%; Score 802; DB 1; Length 157;



```
; Sequence 2, Application US/08217529
; Patent No. 5597899
; GENERAL INFORMATION:
; APPLICANT: Banner, David
; APPLICANT: Lessner, Werner
; APPLICANT: Lotscher, Hansreudt
; APPLICANT: Stuber, Dietrich
; TITLE OF INVENTION: Tumor Necrosis Factor Mutelins
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,529
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; PRIOR APPLICATION NUMBER: EP 93810224.1
; FILING DATE: 29-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Roseman, Catherine R
; REGISTRATION NUMBER: 34240
; REFERENCE/DOCKET NUMBER: 4105/155
; TELEPHONE: (201) 235-6208
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-217-529-2

Query Match          99.8%; Score 802; DB 1; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.6e-79;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VRSSRTPSDKPVAAVYVANOAEQOLMLNRRANALLANGVELNDQLVPSSEGLYLIYS 60
DB 1 VRSSRTPSDKPVAAVYVANOAEQOLMLNRRANALLANGVELNDQLVPSSEGLYLIYS 60
QY 61 QVLEKGGCGPSTHYLLHTHSIRIAVSYQTKVNLISAIRSPQQRTPGAEAKPMXPYPIYL 120
DB 61 QVLEKGGCGPSTHYLLHTHSIRIAVSYQTKVNLISAIRSPQQRTPGAEAKPMXPYPIYL 120
QY 121 GGVFQLEKGDRLSAEINRPDYLDFAESGQYFFGIALL 157
DB 121 GGVFQLEKGDRLSAEINRPDYLDFAESGQYFFGIALL 157

RESULT 5
US-08-318-193-86
; Sequence 86, Application US/08318193
; Patent No. 5641663
; GENERAL INFORMATION:
; APPLICANT: GARVIN, Robert T.
; APPLICANT: MALEK, Lawrence T.
; TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION
; TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
; TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
; TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES
; NUMBER OF SEQUENCES: 91
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,193
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,314
; FILING DATE:
; APPLICATION NUMBER: US 07/224,568
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 18740/116 CACO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-318-193-86

Query Match          99.8%; Score 802; DB 1; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.6e-79;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VRSSRTPSDKPVAAVYVANOAEQOLMLNRRANALLANGVELNDQLVPSSEGLYLIYS 60
DB 1 VRSSRTPSDKPVAAVYVANOAEQOLMLNRRANALLANGVELNDQLVPSSEGLYLIYS 60
QY 61 QVLEKGGCGPSTHYLLHTHSIRIAVSYQTKVNLISAIRSPQQRTPGAEAKPMXPYPIYL 120
DB 61 QVLEKGGCGPSTHYLLHTHSIRIAVSYQTKVNLISAIRSPQQRTPGAEAKPMXPYPIYL 120
QY 121 GGVFQLEKGDRLSAEINRPDYLDFAESGQYFFGIALL 157
DB 121 GGVFQLEKGDRLSAEINRPDYLDFAESGQYFFGIALL 157

RESULT 6
US-08-397-470-1
; Sequence 1, Application US/08397470
; Patent No. 5652353
; GENERAL INFORMATION:
; APPLICANT: Fliers, W.
; APPLICANT: Taverntier, J.
; APPLICANT: Van Ostaede, X.
; TITLE OF INVENTION: TNF-Mutelins
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,470  
FILING DATE: 01-MAR-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/794,400  
FILING DATE: 20-NOV-1991  
APPLICATION NUMBER: EP 90810901.0  
FILING DATE: 21-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Krovatin, William  
REGISTRATION NUMBER: 33256  
REFERENCE/DOCKET NUMBER: 4105/136-00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201) 235-4387  
TELEFAX: (201) 235-3500  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
TISSUE TYPE: Blood  
CELL TYPE: Macrophage  
US-08-397-470-1

Query Match 99.8%; Score 802; DB 1; Length 157;  
Best Local Similarity 99.4%; Pred. No. 2.6e-79;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VRSSRTPSDKPYAHVAVNPQAEQQLQWLNRRANALLANGVELRDQNLVVPSEGLYIYS 60  
DB 1 VRSSRTPSDKPYAHVAVNPQAEQQLQWLNRRANALLANGVELRDQNLVVPSEGLYIYS 60  
QY 61 QVLFKGGCGPSTHVLLTHRTISRIAVSYQTKVNLLSAIKSPCQRETEPGAARPMWEPYIL 120  
DB 61 QVLFKGGCGPSTHVLLTHRTISRIAVSYQTKVNLLSAIKSPCQRETEPGAARPMWEPYIL 120  
QY 121 GGVFQLEKGDRLSAEINRPDYLDFAESGOVYFGIIAL 157  
DB 121 GGVFQLEKGDRLSAEINRPDYLDFAESGOVYFGIIAL 157

RESULT 7  
US-08-192-102-1  
Sequence 1, Application US/08192102  
Patent No. 5656272  
GENERAL INFORMATION:  
APPLICANT: Le, Junming  
APPLICANT: Vilcek, Jan  
APPLICANT: Daddona, Peter E.  
APPLICANT: Ghayeb, John M.  
APPLICANT: Knight, David M.  
APPLICANT: Siegel, Scott A.  
TITLE OF INVENTION: ANTI-TNF ANTIBODIES AND ASSAYS EMPLOYING  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/192,102  
FILING DATE: 04-FEB-1994  
CLASSIFICATION: 424  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/08/192,093  
FILING DATE: 04-FEB-1994  
APPLICATION NUMBER: US 08/013,413  
FILING DATE: 02-FEB-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/010,406  
FILING DATE: 29-JAN-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/943,852  
FILING DATE: 11-SEP-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/853,606  
FILING DATE: 18-MAR-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/670,827  
FILING DATE: 18-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: NY093-01M3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-192-102-1

Query Match 99.8%; Score 802; DB 1; Length 157;  
Best Local Similarity 99.4%; Pred. No. 2.6e-79;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VRSSRTPSDKPYAHVAVNPQAEQQLQWLNRRANALLANGVELRDQNLVVPSEGLYIYS 60  
DB 1 VRSSRTPSDKPYAHVAVNPQAEQQLQWLNRRANALLANGVELRDQNLVVPSEGLYIYS 60  
QY 61 QVLFKGGCGPSTHVLLTHRTISRIAVSYQTKVNLLSAIKSPCQRETEPGAARPMWEPYIL 120  
DB 61 QVLFKGGCGPSTHVLLTHRTISRIAVSYQTKVNLLSAIKSPCQRETEPGAARPMWEPYIL 120  
QY 121 GGVFQLEKGDRLSAEINRPDYLDFAESGOVYFGIIAL 157  
DB 121 GGVFQLEKGDRLSAEINRPDYLDFAESGOVYFGIIAL 157

RESULT 8  
US-08-324-799-1  
Sequence 1, Application US/08324799  
Patent No. 5698195  
GENERAL INFORMATION:  
APPLICANT: Le, Junming  
APPLICANT: Vilcek, Jan  
APPLICANT: Daddona, Peter E.  
APPLICANT: Ghayeb, John M.  
APPLICANT: Knight, David M.  
APPLICANT: Siegel, Scott A.  
TITLE OF INVENTION: ANTI-TNF ANTIBODIES AND PEPTIDES  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive





Db 61 QVLFKGGCSTHVLTHRTISRIAVSYQTKVNLISAIKSPCQRETPGAEAKPWEPYTL 120  
QY 121 GGVEFQLEKGDRLSAEINRPDYLDFAESGQVYFGIAL 157  
Db 121 GGVEFQLEKGDRLSAEINRPDYLDFAESGQVYFGIAL 157

RESULT 10  
US-08-394-600B-17  
; Sequence 17, Application US/08394600B  
; Patent No. 5843693  
; GENERAL INFORMATION:  
; APPLICANT: Halebeck, Robert F.  
; APPLICANT: Jewell, David A.  
; APPLICANT: Kochs, Kirston E.  
; APPLICANT: Krieglner, Michael  
; APPLICANT: Perez, Carl  
; TITLE OF INVENTION: Compositions for the inhibition of  
; TITLE OF INVENTION: Protein Hormone Formation and Uses Thereof  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th Floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: 02/27/95  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Donald J. Pochopien  
; REGISTRATION NUMBER: 32,167  
; REFERENCE/DOCKET NUMBER: 820.005/118500S05  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9135  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-394-600B-17

Query Match 99.8%; Score 802; DB 2; Length 157;  
Best Local Similarity 99.4%; Pred. No. 2.6e-79;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VSSSRTPSDKPYAHVYVNPQAEQQLQWLNRANALLANGVELRDQLVVPSGGLYLI 60  
Db 1 VSSSRTPSDKPYAHVYVNPQAEQQLQWLNRANALLANGVELRDQLVVPSGGLYLI 60  
QY 61 QVLFKGGCSTHVLTHRTISRIAVSYQTKVNLISAIKSPCQRETPGAEAKPWEPYTL 120  
Db 61 QVLFKGGCSTHVLTHRTISRIAVSYQTKVNLISAIKSPCQRETPGAEAKPWEPYTL 120  
QY 121 GGVEFQLEKGDRLSAEINRPDYLDFAESGQVYFGIAL 157  
Db 121 GGVEFQLEKGDRLSAEINRPDYLDFAESGQVYFGIAL 157

RESULT 11  
US-08-500-860A-35  
; Sequence 35, Application US/08500860A

; Patent No. 5891679  
; GENERAL INFORMATION:  
; APPLICANT: LUCAS, RUDOLPH  
; APPLICANT: DE BATESLIER, PATRICK  
; APPLICANT: FRANKEN, LUCIE  
; APPLICANT: SABLOM, ERWIN  
; TITLE OF INVENTION: TNF-MUTAINS, A PROCESS FOR PREPARING THEM AND  
; TITLE OF INVENTION: THEIR USE AS ACTIVE SUBSTANCES IN PHARMACEUTICAL COMPOSITIO  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHUYE P. C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/500,860A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BYRNE, THOMAS E.  
; REGISTRATION NUMBER: 32,205  
; REFERENCE/DOCKET NUMBER: 1487-8  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)816-4000  
; TELEFAX: (703)816-4100  
; TELEX: 200797 NIXN UR  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-500-860A-35

Query Match 99.8%; Score 802; DB 2; Length 157;  
Best Local Similarity 99.4%; Pred. No. 2.6e-79;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VSSSRTPSDKPYAHVYVNPQAEQQLQWLNRANALLANGVELRDQLVVPSGGLYLI 60  
Db 1 VSSSRTPSDKPYAHVYVNPQAEQQLQWLNRANALLANGVELRDQLVVPSGGLYLI 60  
QY 61 QVLFKGGCSTHVLTHRTISRIAVSYQTKVNLISAIKSPCQRETPGAEAKPWEPYTL 120  
Db 61 QVLFKGGCSTHVLTHRTISRIAVSYQTKVNLISAIKSPCQRETPGAEAKPWEPYTL 120  
QY 121 GGVEFQLEKGDRLSAEINRPDYLDFAESGQVYFGIAL 157  
Db 121 GGVEFQLEKGDRLSAEINRPDYLDFAESGQVYFGIAL 157

RESULT 12  
US-08-192-861A-1  
; Sequence 1, Application US/08192861A  
; Patent No. 5919452  
; GENERAL INFORMATION:  
; APPLICANT: Le, Junning  
; APPLICANT: Vilcek, Jan  
; APPLICANT: Daddona, Peter E.  
; APPLICANT: Grayeb, John  
; APPLICANT: Knight, David M.  
; APPLICANT: Siegel, Scott A.  
; TITLE OF INVENTION: METHODS OF TREATING TNF-MEDIATED DISEASE USING  
; TITLE OF INVENTION: CHIMERIC ANTI-TNF ANTIBODIES (As Amended)



QY 121 GGVFQLEKGRSLAEINRPDYLDFAESGQVYFGIIL 157  
Db 121 GGVFQLEKGRSLAEINRPDYLDFAESGQVYFGIIL 157

RESULT 14  
US-08-584-031-13  
; Sequence 13, Application US/08584031A  
; Patent No. 6030945  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: APO-2 LIGAND  
; FILE REFERENCE: 11669.220S03  
; CURRENT APPLICATION NUMBER: US/08/584,031A  
; CURRENT FILING DATE: 1996-01-09  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-584-031-13

Query Match 99.8%; Score 802; DB 3; Length 157;  
Best Local Similarity 99.4%; Pred. No. 2.6e-79;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 VRSSRRPSDKPVAVYVYANPQAEQOLWLNRRANALLANGVELDNDQLVVPSSEGLYLIYS 60  
Db 1 VRSSRRPSDKPVAVYVYANPQAEQOLWLNRRANALLANGVELDNDQLVVPSSEGLYLIYS 60  
QY 61 QVLEKGGCCPSTHVLTHRTISRIVSYQTKVNLSTAIKSPCQRETPEGAEKPMXEPIYL 120  
Db 61 QVLEKGGCCPSTHVLTHRTISRIVSYQTKVNLSTAIKSPCQRETPEGAEKPMXEPIYL 120  
QY 121 GGVFQLEKGRSLAEINRPDYLDFAESGQVYFGIIL 157  
Db 121 GGVFQLEKGRSLAEINRPDYLDFAESGQVYFGIIL 157

RESULT 15  
US-08-714-960B-1  
; Sequence 1, Application US/08714960B  
; Patent No. 6121237  
; GENERAL INFORMATION:  
; APPLICANT: RATHJEN, Deborah A  
; TITLE OF INVENTION: Neutrophil Stimulating Peptides  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER & WITCOFF, LTD.  
; STREET: 10 S. Wacker Drive, Suite 3000  
; City: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 1.44 Mb storage diskette, 3.50 inch  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: IBM compatible PC/MS-DOS  
; SOFTWARE: WordPerfect version 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/714,960B  
; FILING DATE: 17-SEP-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU P39065  
; FILING DATE: 12-MAR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/AU91/00086  
; FILING DATE: 12-MAR-1991  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/930,415  
FILING DATE: 09-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/107,235  
FILING DATE: 16-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Resis, Robert H.  
REGISTRATION NUMBER: 32,168  
REFERENCE/DOCKET NUMBER: 92,622-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 715-1000  
TELEFAX: (312) 715-1234  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..157  
OTHER INFORMATION: /note="Human TNF"  
US-08-714-960B-1

Query Match 99.8%; Score 802; DB 3; Length 157;  
Best Local Similarity 99.4%; Pred. No. 2.6e-79;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 VRSSRRPSDKPVAVYVYANPQAEQOLWLNRRANALLANGVELDNDQLVVPSSEGLYLIYS 60  
Db 1 VRSSRRPSDKPVAVYVYANPQAEQOLWLNRRANALLANGVELDNDQLVVPSSEGLYLIYS 60  
QY 61 QVLEKGGCCPSTHVLTHRTISRIVSYQTKVNLSTAIKSPCQRETPEGAEKPMXEPIYL 120  
Db 61 QVLEKGGCCPSTHVLTHRTISRIVSYQTKVNLSTAIKSPCQRETPEGAEKPMXEPIYL 120  
QY 121 GGVFQLEKGRSLAEINRPDYLDFAESGQVYFGIIL 157  
Db 121 GGVFQLEKGRSLAEINRPDYLDFAESGQVYFGIIL 157

Search completed: August 30, 2002, 17:36:34  
Job time: 627 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2002, 17:31:12 ; Search time 16.71 Seconds  
(without alignments)  
902.814 Million cell updates/sec

Title: US-09-981-289A-20

Perfect score: 804

Sequence: 1 VRSSSRFTSDKPKVAHVAVNP.....RPDYLPFAESGQVFGIITL 157

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	802	99.8	233	1 QMHUN	tumor necrosis fac
2	795	98.9	233	1 S22052	tumor necrosis fac
3	728	90.5	233	2 S11688	tumor necrosis fac
4	720	89.6	234	1 JQ1344	tumor necrosis fac
5	698.5	86.9	232	1 S12606	tumor necrosis fac
6	657.5	81.8	235	1 QWMSN	tumor necrosis fac
7	652	81.1	185	2 S52715	tumor necrosis fac
8	652	81.1	233	1 S24642	tumor necrosis fac
9	651.5	80.0	235	2 S15490	tumor necrosis fac
10	650	80.8	234	1 JH0529	tumor necrosis fac
11	645.5	80.3	193	2 S06192	tumor necrosis fac
12	643.5	80.0	234	1 A25451	tumor necrosis fac
13	642.5	79.9	235	2 JU0029	tumor necrosis fac
14	265.5	33.0	197	1 JH0309	tumor necrosis fac
15	259.5	32.3	204	1 S24641	lymphotoxin - bovl
16	254.5	31.7	204	1 S17289	tumor necrosis fac
17	247	30.7	202	1 JN0869	tumor necrosis fac
18	244.5	30.4	202	1 B27103	tumor necrosis fac
19	218.5	27.2	205	1 QWHDV	lymphotoxin alpha
20	175.5	21.8	278	2 A49266	Fas ligand - rat
21	173.5	20.1	279	2 A53062	Fas ligand - mouse
22	162	20.6	244	2 A46066	lymphotoxin beta -
23	158	19.7	281	2 I38707	Fas ligand - human
24	132	16.4	306	2 I49139	lymphotoxin-beta -
25	125	15.5	260	2 S21738	CD40 ligand - mous
26	121	15.0	261	2 I53476	CD40 ligand - huma
27	117	14.6	261	2 S53090	complement C5 prec
28	78	9.7	1680	1 C5MS	hypothetical prote
29	76.5	9.5	213	2 AF2283	

30	76	9.5	430	2 AG2256	dihydrolipeamide S
31	75.5	9.4	887	2 AD2009	hypothetical prote
32	74.5	9.3	288	2 A83443	probable transcrip
33	74	9.2	799	2 C82929	ATP synthase alpha
34	73.5	9.1	385	2 AH2269	heterocyst specifl
35	73.5	9.1	993	2 G84632	probable GntR-fam1
36	73	9.1	230	2 A95354	CD30 ligand - huma
37	73	9.1	234	2 A40710	D2007.2 protein -
38	72	9.0	195	2 S44788	conserved hypochet
39	72	9.0	386	2 B75516	hypothetical prote
40	72	9.0	4077	2 T17484	surface antigen CD
41	71	8.8	193	2 A40738	hypothetical prote
42	71	8.8	265	2 B84108	sapc protein homol
43	71	8.8	295	2 C64134	hypothetical prote
44	70.5	8.7	217	2 F86343	hypothetical prote
45	70	8.7	167	2 B71553	

#### ALIGNMENTS

RESULT 1  
QMHUN  
tumor necrosis factor alpha precursor [validated] - human  
N:Alternate names: cachectin; TNFA  
C:Species: Homo sapiens (man)  
C>Date: 28-Aug-1985 #sequence, revision 28-Aug-1985 #text, change 08-Dec-2000  
C:Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; A01646;  
R:Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica  
Nucleic Acids Res. 13, 6361-6373, 1985  
A:Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and c  
A:Reference number: A93585; MUID:86016093  
A:Accession: A93585  
A:Molecule type: DNA  
A:Residues: 1-233 <NED>  
A:Cross-references: GB:X02910; GB:X02159; NID:g377209; PIDN:CAA26669.1; PID:g37210  
R:Irish, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Petrof, V.; Ju  
Nature Genet. 3, 137-145, 1993  
A:Title: Dense Alu clustering and a potential new member of the NFkappaB family with  
A:Reference number: S36152; MUID:93272029  
A:Accession: S36153  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-233 <IRI>  
A:Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAAT8745.1; PID:g37212  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992  
R:Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M  
Nature 312, 724-729, 1984  
A:Title: Human tumour necrosis factor: precursor structure, expression and homology t  
A:Reference number: A93351; MUID:85086244  
A:Accession: A93351  
A:Molecule type: mRNA  
A:Residues: 1-233 <PEN>  
A:Cross-references: GB:X02910; GB:X02159; NID:g377209; PIDN:CAA26669.1; PID:g37210  
A>Note: this protein was isolated from the monocytic-like cell line HL-60 from a promy  
R:Meng, A.M.; Cressley, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdel, J.N  
Science 228, 149-154, 1985  
A:Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.  
A:Reference number: A44189; MUID:85142190  
A:Accession: A44189  
A:Molecule type: mRNA  
A:Residues: 1-62, 'S', 64-233 <MAN>  
A:Cross-references: GB:M10968; NID:g339737; PIDN:AAA61198.1; PID:g339738  
R:Fukuda, S.; Ando, S.; Sanou, O.; Tanaka, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.;  
Lymphokine Res. 7, 175-185, 1988  
A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta  
A:Reference number: A61478; MUID:88301617  
A:Accession: B61478  
A:Molecule type: Protein  
A:Residues: 83-102;109-119;121-128, 'X', 130-131;142-144, 'X', 146, 'XXX', 150-152;159-174;  
R:Marmentout, A.; Franssen, L.; Tavernier, J.; Van Der Heyden, J.; Tilard, R.; Kawashim  
Eur. J. Biochem. 152, 515-522, 1985  
A:Title: Molecular cloning and expression of human tumor necrosis factor and comparis

A:Accession: 153311; MUID:86030296  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-233 <MAR>  
A:Cross-references: GB:M26331; NID:9339763; PID:AAA36758.1; PID:9339764  
A:Experimental source: U-937 cells  
R:Takekura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.  
E:J. Biochem. 235, 431-437, 1996  
A:Title: O-6-glycosylated species of natural human tumor-necrosis factor-alpha.  
A:Reference number: S62610; MUID:96202967  
A:Accession: S62610  
A:Molecule type: protein  
A:Residues: 77-99 <TAK>  
R:D'Alfonso, S.; Richiardi, P.M.  
Immunogenetics 39, 150-154, 1994  
A:Title: A polymorphic variation in a putative regulation box of the TNFA promoter region  
A:Reference number: I54522; MUID:94102809  
A:Accession: I54522  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-8 <DAL>  
A:Cross-references: GB:S68530; NID:9544751  
R:Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.  
J. Exp. Med. 176, 1053-1062, 1992  
A:Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lysines  
A:Reference number: A59163; MUID:93018820  
A:Contents: annotation: identification of myristylated lysines  
R:Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Bring  
J. Biol. Chem. 260, 2345-2354, 1985  
A:Title: Human tumor necrosis factor. Production, purification, and characterization.  
A:Reference number: A92511; MUID:8510974  
A:Contents: annotation: disulfide bond  
C:Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction  
out detriment to normal cells. It can also act synergistically with interferon gamma to  
C:Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes closely  
ut are produced by different cell types and have different induction kinetics.  
C:Genetics:  
A:Gene: GDB: TNF; TNFA  
A:Cross-references: GDB:120441; OMIM:191160  
A:Map position: 6p21.3-6p21.3  
A:Introns: 62/3; 78/1; 94/1  
C:Complex: homotrimer  
C:Superfamily: tumor necrosis factor  
C:Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; macr  
F:1-76/Domains: propeptide #status predicted <PRO>  
F:77-233/Product: tumor necrosis factor #status experimental <MAR>  
F:19,20/Binding site: myristate (lys) (covalent) #status experimental  
F:81/Binding site: carboxylate (Ser) (covalent) (partial) #status experimental  
F:145-177/Disulfide bonds: #status experimental

Query Match	99.8%	Score 802;	DB 1;	Length 233;
Best Local Similarity	99.4%;	Pred. No. 9.96-76;		
Matches 156;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY 1	VSSSSRTPSDKPAHVAVANPOAESQLOMLNRRANALLANGVELRNOLVVPSEGLYLIIS	60		
DB 77	VSSSSRTPSPKPAHVAVANPOAESQLOMLNRRANALLANGVELRNOLVVPSEGLYLIIS	136		
QY 61	QVLFKSGCGPSTHVLLTHTTSRIAVSYOTKNNLSAISKPOCRETPEGAAPKWPXEPYIL	120		
DB 137	QVLFKSGCGSTHVLLTHTTSRIAVSYOTKNNLSAISKPOCRETPEGAAPKWPXEPYIL	196		
QY 121	GGVFOLEKGDRLSAETNRPDYLDFAESGQVFFGIATL	157		
DB 197	GGVFOLEKGDRLSAETNRPDYLDFAESGQVFFGIATL	233		

RESULT 2  
572052  
tumor necrosis factor alpha precursor - baboon  
C:Species: Papio sp.(baboon)

C.Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000  
C.Accession: S22052  
C.Sanjanwala, M.; Edwards, A.  
submitted to the EMBL Data Library, September 1991  
A.Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genom  
A.Reference number: S22052  
A.Accession: S22052  
A.Status: preliminary  
A.Molecule type: DNA  
A.Residues: 1-233 <S&N>  
A.Cross-references: EMBL:X62141; NID:g38159; PIDN:CAA44068.1; PID:g38160  
C.Genetics:  
A.Introns: 62/3; 78/1; 94/1  
C.Superfamily: tumor necrosis factor  
C.Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein  
F19/20/Binding site: myristate (lys) (covalent) #status predicted  
F181/Binding site: carboxylate (Ser) (covalent) #status predicted  
F145-177/Disulfide bonds: #status predicted

Query Match	98.98%	Score 795	DB 1	Length 233
Best Local Similarity	98.78%	Pred. No. 5.3e-75		
Matches 155	Conservative	0	Mismatches 2	Indels 0
QY	1 VSSRSRTPSDKRVAAHVANPQAEGLQWIMRRANMLANGVELRDNLQVPSSEGLYLIS	60		
Db	77 VASSRSTPDKRVAAHVANPQAEGLQWIMRRANMLANGVELRDNLQVPSSEGLYLIS	136		
QY	61 QVLFKGGCGPSTHVLLTHTTISRIVASYOTKVNLLSAIKSPCORETPEGAEAKPMKEPIYL	120		
Db	137 QVLFKGGCGPSTHVLLTHTTISRIVASYOTKVNLLSAIKSPCORETPEGAEAKPMKEPIYL	196		
QY	121 GGVFQLEKGRDLSAEINRPDIYLDFAESGVYRGIIAL	157		
Db	197 GGVFQLEKGRDLSAEINRPDIYLDFAESGVYRGIIAL	233		

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RESULT 3
S11688
tumor necrosis factor alpha precursor - cat
C:Species: Felis silvestris catus (domestic cat)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Feb-2000
C:Accession: S11688
R:McGraw, R.A.: Coffee, B.W.: Otto, C.M.: Drews, R.T.: Rawlings, C.A.
Nucleic Acids Res. 18, 5563, 1990
A:Title: Gene sequence of feline tumor necrosis factor alpha.
A:Reference number: S11688; M0ID:91016860
A:Accession: S11688
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-233 <MGCG>
A:Cross-references: EMBL:X54000; NID:g1084; PIDN:CA437948.1; PID:g255777
C:Genetics:
A:Introns: 62/3; 78/1; 94/1
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F:19,20/Binding site: myristate (lys) (covalent) #status predicted
F:81/Binding site: carboxylate (Ser) (covalent) #status predicted
F:145-177/Disulfide bonds: #status predicted

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	Query Match	90.5%	Score 728;	DB 2:	Length 233;
	Best Local Similarity	91.1%;	Pred. No.	4.9e-68;	
	Matches 143; Conservative	4;	Mismatches	10;	Indels 0; Gaps 0;
QY	1 VSSSRKTPEDKVAHVAVNPAEQGLQWLNRANMLLVANGVELRDNLQVVPSEGLYLIS	60			
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :				
Dd	77 LRSSSTPTSDKPVAAHVAVNPAAEGQLQRSLRRANMLLVAGVELTQNQLVPDGDLYLIS	136			
QY	61 QVLFFKGCGCPSTHVLTHTRISRILANSIQCKNVLLSAIKSPQCRREPPEGAEAPWLEPYTL	120			
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :				
Dd	137 QVLFQGQGGPSTHVLTHAISRFPAVSQTCKNVLLSAIKSPCCORETPEGAEPWLEPYTL	196			



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A:Molecule type: DNA
A:Residues: 1-235 <SEM>
A:Cross-references: GB:X00467; NID:g54830; PIDN:CAA68530.1; PID:g54832
R:pennica, D.; Hayflick, J.S.; Bringham, T.S.; Palladino, M.A.; Goeddel, D.V.
Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985
A>Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necrosis factor
A:Reference number: A25164; MWID:85298296
A:Accession: A25164
A:Molecule type: mRNA
A:Residues: 1-235 <PEN>
A:Cross-references: GB:M11731; NID:g202084; PIDN:AAA40458.1; PID:g202085
R:Franzen, L.; Muller, R.; Matmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashima,
Nucleic Acids Res. 13, 4417-4429, 1985
A>Title: Molecular cloning of mouse tumor necrosis factor cDNA and its eukaryotic expres
A:Reference number: A23127; MWID:85242112
A:Accession: A23127
A:Molecule type: mRNA
A:Residues: 1-235 <RA>
A:Cross-references: GB:X02611; NID:g54844; PIDN:CAA26457.1; PID:g54845
R:Csehn, K.; Beutler, B.
J. Biol. Chem. 264, 16256-16260, 1989
A>Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide results
A:Reference number: A34251; MWID:89380231
A:Accession: A34251
A:Molecule type: protein
A:Residues: 70-87 <CSE>
R:Caputi, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986
A>Title: Identification of a common nucleotide sequence in the 3'-untranslated region of
A:Reference number: I59058; MWID:86149365
A:Accession: I59058
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-230, 'R', 232-235 <RES>
A:Cross-references: GB:M13049; NID:g202082; PIDN:AAA40457.1; PID:g202083
R:Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.
Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990
A>Title: Characterization of high molecular weight glycosylated forms of murine tumor ne
A:Reference number: A36696; MWID:9109531
A:Accession: A36696
A:Molecule type: protein
A:Residues: 80-85, 'X', 87-99 <SHE>
C:Genetics:
A:Introns: 62/3; 81/1; 97/1
A>Note: the first intron occurs in the 5'-untranslated region
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytoloxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
F:80-235/Product: tumor necrosis factor #status experimental <MAT>
F:20/Binding site: myristate (Lys) (covalent) #status predicted
F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:86/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:146-179/Disulfide bonds: #status predicted

Query Match      81.8%; Score 657.5; DB 1; Length 235;
Best Local Similarity 78.3%; Pred. No. 1,le-60;
Matches 123; Conservative 20; Mismatches 13; Indels 1; Gaps 1;

QY 1 VSSSRTPSDKPAHVAVANPOAESQLQMLNRANAALLANGVELRDNLVVPSEGILYIS 60
    ||||| :||||| | | | | :||||| :| :||||| :| :|||
Db 80 LRSSSNSSNSSPKAHVAVANQVEOLEWLSORANVALLANGMDLKDNQIVPPADGLTYVS 139
    ||||| :||||| :| :||| :| :||| :||| :||| :||| :|||
QY 61 QYLEFKGGCGSTVLLTHTTSIRIAVSOTKNLSAISIPQOREPPEGAEARPMXPPIYL 120
    ||||| :||||| :| :||| :| :||| :||| :||| :||| :|||
Db 140 QYLEFKGGCGCD-VLLLTHTVSREFAISTOEKYNLLSAVKSPEKPDPEGAELKPWEPIYL 198
    ||||| :||||| :| :||| :| :||| :||| :||| :||| :|||
QY 121 GGVFQLEKGDRLSAEINRPDIYLDPAESGQGVFGIATL 157
    ||||| :||||| :| :||| :| :||| :||| :||| :||| :|||
Db 199 GGVFQLEKGDRQLSAEVLNPKYIDPAESGQGVFYAL 235

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tumor necrosis factor alpha precursor - bovine (fragment)  
C.Species: Bos primigenius taurus (cattle)  
C.Date: 19-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 04-Feb-2000  
C.Accession: S52715  
R.Mertens, B.; Gaidulis, L.  
submitted to the EMBL Data Library, March 1995  
A.Description: Cloning and sequence analysis of cDNAs encoding bovine CD40 ligand and  
A.Reference number: S52715  
A.Accession: S52715  
A.Status: preliminary  
A.Molecule type: mRNA  
A.Residues: 1-185 <MEM>  
A.Cross-references: EMBL:Z48808; NID:9755701; PIDN:CAA8743.1; PID:9755702  
C.Superfamily: tumor necrosis factor  
C.Keywords: glycoprotein  
F.33/Binding site: carbohydrate (Ser) (covalent) #status predicted  
F.97-129/Disulfide bonds: #status predicted

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Query Match Similarity 81.1%; Score 652; DB 2; Length 185;
Best Local Similarity 80.3%; Pred. No. 3.9e-60;
Matches 126; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 VSSSRTPESDKPVAHVAVNPOAEGQLWLNRRANALLANGVELRDNLVPESEGLYLYIS 60
   ||||| : ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| :
DB 29 LRSSSQASSNKRVAHVAVDINSFGLRWMDSYANALLMANGVKLEBNOQLVVPADGLYLYIS 88
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 61 QVLFEGGCGCPSTPLFTHTISRIVSYOTKYNLSAISKPCQRETPEGAEAKPMXEPYIL 120
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
DB 89 QVLFEGGCGCPSTPLFTHTISRIVSYOTKYNLSAISKPCRHRETPWEAEAKPMYEPYIQ 148
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 121 GGVPLEKGRDLRAEINRPDYLDFAESGOVYFGIALL 157
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
DB 149 GGVFQLEKGRDLRAEINLPDYLDFAESGOVYFGIALL 185
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :

RESULT 8
S24642
tumor necrosis factor alpha precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: I46047; S24642
R:Clndts, I.; Cleuter, Y.; Kettmann, R.; Burry, A.; Droogmans, L.
cytokine 5, 336-341, 1993
A:Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and
A:Reference number: I46046; MUID:94083525
A:Accession: I46047
A:Status: preliminary; translated from GR/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-233 <CL2>
A:Cross-references: EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798
C:Genetics:
A:Gene: TNFA
A:Introns: 62/3; 78/1; 94/1
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F:20/Binding site: myristate (lys) (covalent) #status predicted
F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:145-177/Disulfide bonds: #status predicted

Query Match 81.1%; Score 652; DB 1; Length 233;
Best Local Similarity 80.3%; Pred. No. 3.9e-60;
Matches 126; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 VSSSRTPESDKPVAHVAVNPOAEGQLWLNRRANALLANGVELRDNLVPESEGLYLYIS 60
   ||||| : ||||| : ||| : ||||| : ||||| : ||||| : ||||| : ||||| :
DB 77 LRSSSQASSNKRVAHVAVDINSFGLRWMDSYANALLMANGVKLEBNOQLVVPADGLYLYIS 136
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 61 QVLFEGGCGCPSTPLFTHTISRIVSYOTKYNLSAISKPCQRETPEGAEAKPMXEPYIL 120
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
DB 137 QVLFEGGCGCPSTPLFTHTISRIVSYOTKYNLSAISKPCRHRETPWEAEAKPMYEPYIQ 196
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :

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Qy 121 GGVFQLEKGRLSAEINRPDYLDFAESGGVYFGIIAL 157
    |||||
Db 197 GGVFQLEKGRLSAEINRPDYLDYAESGGVYFGIIAL 233
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RESULT 9  
154490  
tumor necrosis factor alpha precursor - white-footed mouse  
C:Species: Peromyscus leucopus (white-footed mouse)  
C:Date: 02-Aug-1996 #sequence.revision 02-Aug-1996 #text.change 04-Feb-2000  
C:Accession: 154490  
R:Crew, M.D.; Filipowsky, M.E.  
Immunogenetics 35: 351-353, 1992  
A:Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leucopus  
A:Reference number: 154490; MUID:92218012  
A:Accession: 154490  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-235 <RES>  
A:Cross-references: GB:M59233; NID:g202506; PIDN:AAA0596.1; PID:g202507  
C:Genetics:  
A:Gene: P1TNF  
A:Introns: 62/3; 81/1; 97/1  
C:Superfamily: tumor necrosis factor  
C:Keywords: glycoprotein; lipoprotein; myristylation  
E:19,20/Binding site: myristate (Tys) (covalent) #status predicted  
E:84/Binding site: carboxylate (Ser) (covalent) #status predicted

	Query Match	81.0%;	Score 651.5;	DB 2:	Length 235;
	Best Local Similarity	78.3%;	Pred. No. 4.4e-60;		
	Matches 123;	Conservative 20;	Mismatches 13;	Indels 1;	Gaps 1;
QY	1 VRSSRTPSDPRVAHVYVANPQAEGLQWLNRRANALLANGVELRDNLQVPESEGLLYLS 60				
Db	80 LRSSQNSSDKPRVAHVYVANQVDELEWLSGANNALLANGMDLKNQLYIPADGXYLYLS 139				
QY	61 QVLEKGGCCSTHVLHTHTISRIASVYOTKYNLLSAIKSPCORETEPEGAEAKPMXEPYTL 120				
Db	140 QVLEKGGCC-SSYVLLHTHTVSRFANSYEDKYNLLSAIKSPCKETPEGESSELPKPMYEPYTL 198				
QY	121 GGVFQLEKGRDLASAINRPDLDPAESQVYFGITAL 157				
Db	199 GGVFQLEKGRDLASAINRPDLDPAESQVYFGITAL 235				

RESULT 10  
JH0529  
tumor necrosis factor alpha precursor - sheep  
N:Alternate names: cachectin; TNF alpha  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 10-Sep-1999 #sequence.revision 10-Sep-1999 #text\_change 04-Feb-2000  
C:Accession: JH0529; S48118; S13114; S20661  
R:Green, I.R.; Sargan, D.R.  
Gene 109, 203-210, 1991  
A:Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems with  
A:Reference number: JH0529; MUID:92112044  
A:Accession: JH0529  
A:Molecule type: mRNA  
A:Residues: 1-234 <GRE>  
A:Cross-references: EMBL:X5152; NID:91405; PIDN:CAA38952.1; PID:91406  
A:Experimental source: alveolar macrophage  
A:Nash, A.D.; Barcham, G.J.; Brandon, M.R.; Andrews, A.E.  
Immunol. Cell Biol. 69, 273-283, 1991  
A:Title: Molecular cloning, expression and characterization of ovine TNF-alpha.  
A:Reference number: S48118; MUID:92155784  
A:Accession: S48118  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-234 <NMS>  
A:Cross-references: EMBL:X56756; NID:9297806; PIDN:CAA0076.1; PID:9297807  
R:Youn, A.J.; Hay, J.B.; Chan, J.Y.C.  
Nucleic Acids Res. 18, 6723, 1990

A:Title: Primary structure of ovine tumor necrosis factor alpha cDNA.  
A:Reference number: S13114; MUID:91067496  
A:Accession: S13114  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-62,64-734 <TUN>  
A:Cross-references: EMBL:X55966; MID:g1403; PIDN:CA439437.1; PID:g1404  
A:Note: comparison with the introns of homologous sequences suggest that this is prob  
C:Superfamily: tumor necrosis factor  
C:Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein, lym  
F:1-77/Domain: propeptide #status predicted <PRO>  
F:78-234/Product: tumor necrosis factor alpha #status predicted <TUN>  
F:20/Binding site: myristate (Lys) (covalent) #status predicted  
F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted  
F:96/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:146-178/Disulfide bonds: #status predicted

```

Query Match      80.8%; Score 650; DB 1; Length 234;
Best Local Similarity 80.3%; Pred. No. 6.3e-60;
Matches 126; Conservative 15; Mismatches 16; Indels 0; Gaps 0.

QY 1 VRSSRRPSDRPVAAHVAVNPAQEGQLQMLNRRANALLANGVELRDNLQVVPSEGLYLIYS 60
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 78 LRSSQASNNKPVAAHVAVNANISAPGLRMGDSYANMLANGVELKONQLVPPDGLYLIYS 137

QY 61 QVLEKGGCCPESTHVLHHTISRIAVSYOTKYNLLSAIKSPCORETPEGAEAKPMKEPIYL 120
   ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 138 QVLEFGHCCPESTPELFTHTISRIAVSYOTKYNLLSAIKSPCHRETLLEGAEAKPMKEPIYO 197

QY 121 GGVFQLEKGDRLSAEINRPDYLDFAESQOVYGGIALL 157
   ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 198 GGVFQLEKGDRLSAEINRPDYLDFAESQOVYGGIALL 234

```

RESULT 11  
506192  
tumor necrosis factor alpha precursor - goat (fragment)  
N:Alternate names: cachectin; TNF alpha  
C:Species: Capra aegagrus hircus (domestic goat)  
C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 31-Jan-2000  
A:Accession: 506192; S41867  
R:Goldstein, I.M.; Henner, D.; Talhouk, A.  
submitted to the EMBL Data Library, March 1989  
A:Reference number: 506192  
A:Accession: 506192  
A:Molecule type: mRNA  
A:Residues: 1-193 <COL>  
A:Cross-references: EMBL:X14828; NID:g992; PIDN:CAA32937.1; PID:g993  
R:Rimstad, E.  
submitted to the EMBL Data Library, January 1994  
A:Reference number: S41867  
A:Accession: S41867  
A>Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 36-38, 'S', 40-78, 'A', 80-88, 'N', 90-114, 'Q', 116-123, 'D', 125-144, 'G', 145-173,  
A:Cross-references: EMBL:X77317; NID:g452607; PIDN:CAA54523.1; PID:g452608  
C:Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage; membrane protease  
F:4/Binding site: carbohydrate (ser) (covalent) #status predicted  
F:106-138/Disulfide bonds: #status predicted

```

Query Match      80.3%; Score 645.5; DB 2; Length 193;
Best Local Similarity 80.9%; Pred. No. 1.5e-59;
Matches 127; Conservative 14; Mismatches 15; Indels 1; Gaps

QY 1 VRSSRTSPDKPAHVAVVANAQEGQQLQWLRKRRANALLANGVELRDNLVVPSEGLYIYS 60
      ||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:|||||
Dh 38 LRSSSQASQSNKPAHVAVVANAISAPQLMGDSYANALKANGVELKDQNLVVPPTGGLYIYS 97
      ||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:|||||

QY 61 QVLEKGGCSTHVLTHTISRANVSQTGVNVLISAKSPQQRETPGCAEAKPMEPIYL 120
      ||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:|||||

```





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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2002, 17:36:13 ; Search time 11.95 Seconds

(without alignments)  
508.700 Million cell updates/sec

Title: US-09-981-289a-20

Perfect score: 804  
Sequence: 1 VRSSSRPSPDKPAVHVANP.....RPDYIDFAESGQVYRGIIL 157

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	802	99.8	233	1	TNFA_HUMAN
2	795	98.9	233	1	TNFA_PAPSP
3	784	97.5	233	1	TNFA_MACMU
4	781	97.1	233	1	TNFA_MACFA
5	780	97.0	233	1	TNFA_PAPHU
6	761	94.7	233	1	TNFA_CANFA
7	728	90.5	233	1	TNFA_FELCA
8	720	89.6	234	1	TNFA_HORSE
9	698.5	86.9	232	1	TNFA_PIG
10	660.5	82.2	234	1	TNFA_CAVPO
11	657.5	81.8	235	1	TNFA_MOUSE
12	653	81.2	229	1	TNFA_CEREL
13	652	81.1	233	1	TNFA_BOVIN
14	651.5	81.0	235	1	TNFA_PERLE
15	650	80.8	234	1	TNFA_SHEEP
16	645.5	80.3	193	1	TNFA_CAPI
17	643.5	80.0	235	1	TNFA_RABIT
18	642.5	79.9	235	1	TNFA_RAT
19	627.5	78.0	233	1	TNFA_MARMO
20	595	74.0	233	1	TNFA_MACEU
21	442	55.0	233	1	TNFA_TRIUV
22	265.5	33.0	197	1	TNFB_RABIT
23	259.5	32.3	204	1	TNFB_BOVIN
24	254.5	31.7	204	1	TNFB_PIG
25	253	31.5	201	1	TNFB_MACEU
26	247	30.7	202	1	TNFB_RAT
27	244.5	30.4	202	1	TNFB_MOUSE
28	218.5	27.2	205	1	TNFB_HUMAN
29	175.5	21.8	278	1	FASL_HUMAN
30	173.5	21.6	279	1	FASL_MOUSE
31	168.5	21.0	240	1	TN14_HUMAN
32	162	20.1	244	1	TNFC_HUMAN
33	158	19.7	281	1	FASL_HUMAN

## ALIGNMENTS

RESULT ID	1	TNFA_HUMAN	STANDARD:	PRT:	233 AA.
AC	P01375				
DT	21-JUL-1986	(Rel. 01, Created)			
DT	21-JUL-1986	(Rel. 01, last sequence update)			
DT	01-MAR-2002	(Rel. 41, last annotation update)			
DE	Tumor necrosis factor precursor (TNF-alpha) (Cachectin).				
GN	TNF OR TNFA.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=67217060; PubMed=3555974;				
RA	Nedospasov S.A., Shakhov A.N., Turetskaya R.L., Mett V.A.,				P50592 mus musculu
RA	Aizov M.M., Georgiev G.P., Korobko V.G., Dobrynin V.N.,				P41155 mus musculu
RA	Filippov S.A., Bystron N.S., Boldyreva E.F., Chuvpilo S.A.,				O14788 h tumor nec
RA	Chumakov A.M., Shingarova L.N., Ovchinnikov Y.A.;				O35235 h tumor nec
RT	"Random arrangement of genes coding for tumor necrosis factor (TNF-alpha) and lymphotoxin (TNF-beta) in the human genome.";				P27348 mus musculu
RT	Cold Spring Harb. Symp. Quant. Biol. 51:611-624(1986).				P29965 homo sapien
RL	[2]				O97605 felis silve
RP	SEQUENCE FROM N.A.				O97626 canis fami
RX	MEDLINE=65137896; PubMed=3883195;				P51749 bos taurus
RA	Shiral T., Yamaguchi H., Ito H., Todd C.W., Wallace R.B.;				P50591 homo sapien
RT	"Cloning and expression in Escherichia coli of the gene for human tumor necrosis factor.";				O9wu72 mus musculu
RL	Nature 313:803-806(1985).				O75888 homo sapien
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=66016093; PubMed=2995927;				
RA	Nedwin G.E., Naylor S.L., Sakaguchi A.Y., Smith D.H.;				
RA	Jarrett-Nedwin J., Pennica D., Goeddel D.V., Gray P.W.;				
RT	"Human lymphotoxin and tumor necrosis factor genes: structure, homology and chromosomal localization.";				
RL	Nucleic Acids Res. 13:6361-6373(1985).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=85142190; PubMed=3856324;				
RA	Wang A.M., Creasey A.A., Lader M.B., Lin L.S., Strickler J.,				
RA	van Arsdale J.N., Yamamoto R., Mark D.F.;				
RT	"Molecular cloning of the complementary DNA for human tumor necrosis factor.";				
RL	Science 228:149-154(1985).				
RN	[6]				
RP	SEQUENCE FROM N.A.				

RX MEDLINE=986030296; PubMed=3932069;  
 RA Matmenou A., Franssen L., Tavernier J., van der Heyden J., Tizard R.,  
 RA Kawashima E., Shaw A., Johnson M.J., Semon D., Mueller R.,  
 RA Ruyschaert M.R., van Vliet A., Fiers W.;  
 RT "Molecular cloning and expression of human tumor necrosis factor and  
 RT comparison with mouse tumor necrosis factor.";  
 RT Eur. J. Biochem. 152:515-524(1985).  
 RN [17]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93272029; PubMed=9499947;  
 RA Irits F.J.M., Bougueleret L., Prieur S., Caterina D., Primas G.,  
 RA Perrot V., Jurka J., Rodriguez-Tome P., Claverie J.-M., Dausset J.,  
 RA Cohen D.;  
 RT "Dense Alu clustering and a potential new member of the NF kappa B  
 RT family within a 90 kilobase HLA class III segment.";  
 RT Nat. Genet. 3:137-143(1993).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RX Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,  
 RA Abbsal N., Dickschhoff R., Loretz C., Madan A., Dors M., Young J.,  
 RA Lasky S., Hood L.;  
 RT "Sequence of the human major histocompatibility complex class III  
 RT region.";  
 RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [9]  
 RP SEQUENCE FROM N.A.  
 RX Shima S., Tamiya G., Oka A., Inoko H.;  
 RA "Homo sapiens 2,129,812bp genomic DNA of 6p21.3 HLA class I region.";  
 RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE=89159409; PubMed=2922050;  
 RA Jones E.Y., Stuart D.I., Walker N.P.;  
 RT "Structure of tumour necrosis factor.";  
 RT Nature 338:225-228(1989).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE=91193276; PubMed=1964681;  
 RA Jones E.Y., Stuart D.I., Walker N.P.;  
 RT "The structure of tumour necrosis factor -- implications for  
 RT biological function.";  
 RT J. Cell Sci. Suppl. 13:11-18(1990).  
 RN [12]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).  
 RX MEDLINE=9008932; PubMed=2551905;  
 RA Eck M.J., Sprang S.R.;  
 RT "The structure of tumor necrosis factor-alpha at 2.6-A resolution.  
 RT Implications for receptor binding.";  
 RT J. Biol. Chem. 264:17595-17605(1989).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MUTANT ARG-107.  
 RX MEDLINE=96147459; PubMed=9488135;  
 RA Reed C., Fu Z.Q., Wu J., Xue Y.N., Harrison R.W., Chen M.J.,  
 RA Weber I.T.;  
 RT "Crystal structure of TNF-alpha mutant R31D with greater affinity for  
 RT receptor R1 compared with R2.";  
 RT Protein Eng. 10:1100-1107(1997).  
 RN [14]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF MUTANT M3S.  
 RX MEDLINE=98113178; PubMed=9442056;  
 RA Cha S.S., Kim J.S., Cho H.S., Shin N.K., Jeong W., Shin H.C.,  
 RA Kim Y.J., Hahn J.H., Oh B.H.;  
 RT "High resolution crystal structure of a human tumor necrosis factor-  
 RT alpha mutant with low systemic toxicity.";  
 RT J. Biol. Chem. 273:2153-2160(1998).  
 RN [15]  
 RP MUTAGENESIS.  
 RX MEDLINE=91184128; PubMed=2009860;  
 RA Ostrade X.V., Tavernier J., Prange T., Fiers W.;  
 RT "Localization of the active site of human tumor necrosis factor  
 RT (hTNF) by mutational analysis.";  
 RT EMBO J. 10:827-836(1991).  
 RN [16]

R	P	MRI-STOXYLATION.
RX	RD	MedLine=93018820; PubMed=1402651;
RA	ST	Stevenson F.T., Bursien S.L., Locksley R.M., Lovett D.H.:
RT	FT	"Myristyl acylation of the tumor necrosis factor alpha precursor on specific lysine residues."
RL	J	J. Exp. Med. 176:1053-1062(1992).
CC	-I-	FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE WITH A WIDE VARIETY OF FUNCTIONS; IT CAN CAUSE CYTOLYSIS OR CENTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEKIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN CONDITIONS.
CC	-I-	SUBUNIT: HOMOTRIMER.
CC	-I-	SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM.
CC	-I-	PEM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTEOLYTIC PROCESSING.
CC	-I-	DISEASE: CACHEKIXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTON, AND IS CHARACTERIZED BY GENERAL ILL HEALTH AND MALNUTRITION.
CC	-I-	SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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DR	EMBL	X02910; CAA26669.1; -
DR	EMBL	M16441; AAA61200.1; -
DR	EMBL	X01394; CAA25650.1; -
DR	EMBL	M10988; AAA61198.1; -
DR	EMBL	M26331; AA36758.1; -
DR	EMBL	Z15026; CADI8745.1; -
DR	EMBL	AFL129756; AAD18091.1; -
DR	EMBL	AP000505; BAB63396.1; -
DR	PIR	B23784; OMHUN.
DR	PIR	A44189; A44189.
DR	PIR	S36153; S36153.
DR	PDB	1TNF; 15-JAN-91.
DR	PDB	2TUN; 31-JAN-94.
DR	PDB	1A8M; 17-JUN-98.
DR	PDB	4TSV; 02-MAR-99.
DR	PDB	5TSM; 07-MAY-99.
DR	GlycosultedB	P01375; -
DR	MIM	191160; -
DR	InterPro	IIPR003636; TNF_abc.
DR	InterPro	IIPR000478; TNF_family.
DR	pfam	PF00229; TNF; 1.
DR	PRINTS	PR01234; TNECROSISFCT.
DR	ProDom	PD002012; TNF_abc; 1.
DR	SMART	SM00207; TNF; 1.
DR	PROSITE	PS00251; TNF_1; 1. PS50049; TNF_2; 1.
KW	Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor; Myristate; 3d-structure; Polymorphism.	
FM	PROPEP	1 76
FT	CHAIN	77      233
FT	TRANSMEM	36      56
FT	LIPID	19      19
FT	LIPID	20      20
FT	DISULFD	145     177
FT	VARIANT	94
FT	MUTAGEN	105
FT	MUTAGEN	108
FT	MUTAGEN	112
FT	MUTAGEN	160
FT	MUTAGEN	162
FT	MUTAGEN	167
FT	MUTAGEN	167

Query Match 99.8%; Score 802; DB 1; Length 233;  
 Best Local Similarity 99.4%; Pred. No. 6,3e-78;  
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VRSSSRTPSDKPVAAHVYVAVNPAQEGQLQMLNRRANALLANGVELDNLVPSSEGLYLITS 60  
 |||||||  
 DB 77 VRSSSRTPSDKPVAAHVYVAVNPAQEGQLQMLNRRANALLANGVELDNLVPSSEGLYLITS 136  
 |||||||  
 QY 61 QVLFKGGCCESTHYLLHTTISRIVSYQTKVNLSSAISKPCQRETPEGAEKPKMXPETYL 120  
 |||||||  
 DB 137 QVLFKGGCCESTHYLLHTTISRIVSYQTKVNLSSAISKPCQRETPEGAEKPKMXPETYL 196  
 |||||||  
 QY 121 GGVFQLEKGRLSAEINRPDYLDFAESGQVYFGIALL 157  
 |||||||  
 DB 197 GGVFQLEKGRLSAEINRPDYLDFAESGQVYFGIALL 233

## RESULT 2

TNFA\_PAPSP STANDARD; PRT; 233 AA.  
 AC P33620;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Cachectin).  
 GN TNF OR TNFA.  
 OS Papio sp. (Baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Papio.  
 OX NCBI\_TaxID=61183;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sanjivnala M., Edwards A.;  
 RL Submitted (SEP-1991) to the EMBL/Genbank/DBJ databases.  
 RT FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES. IT IS A CYTOKINE  
 WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF  
 CERTAIN TUMOR CELL LINES. IT IS IMPLICATED IN THE INDUCTION OF  
 CACHEXIA. IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION  
 OR BY STIMULATION OF INTERLEUKIN 1 SECRETION. IT CAN STIMULATE  
 CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN  
 CONDITIONS.  
 CC SUBUNIT: HOMOTRIMER.  
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
 EXTRACELLULAR SOLUBLE FORM.  
 CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY  
 PROTEOLYTIC PROCESSING.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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DR EMBL: X62141; CAA44068.1; -.  
 DR PIR: S22052; S22052.  
 DR HSSP: P01375; 4TSV.  
 DR InterPro: IPR003636; TNF\_abc.  
 DR InterPro: IPR000478; TNF\_family.  
 DR Pfam: PF00229; TNF\_1.  
 DR PRINTS: PR01234; TNECROSISFCT.  
 DR PRODOM: PD002012; TNF\_abc; 1.  
 DR SMART: SM00207; TNF\_1.  
 DR PROSITE: PS00251; TNF\_1; 1.  
 DR PROSITE: PS50049; TNF\_2; 1.  
 KM Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor;  
 KW Myristate.  
 FT PROPEP 1 76 BY SIMILARITY.  
 FT CHAIN 77 233 TUMOR NECROSIS FACTOR.

FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
 FT LIPID 19 19 MYRISTATE (BY SIMILARITY).  
 FT LIPID 20 20 MYRISTATE (BY SIMILARITY).  
 FT DISULFID 145 177 BY SIMILARITY.  
 SQ SEQUENCE 233 AA; 25557 MW; 45360848DC74173 CRC64;

Query Match 98.9%; Score 795; DB 1; Length 233;  
 Best Local Similarity 98.7%; Pred. No. 3.5e-77;  
 Matches 155; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VRSSSRTPSDKPVAAHVYVAVNPAQEGQLQMLNRRANALLANGVELDNLVPSSEGLYLITS 60  
 |||||||  
 DB 77 VRSSSRTPSDKPVAAHVYVAVNPAQEGQLQMLNRRANALLANGVELDNLVPSSEGLYLITS 136  
 |||||||  
 QY 61 QVLFKGGCCESTHYLLHTTISRIVSYQTKVNLSSAISKPCQRETPEGAEKPKMXPETYL 120  
 |||||||  
 DB 137 QVLFKGGCCESTHYLLHTTISRIVSYQTKVNLSSAISKPCQRETPEGAEKPKMXPETYL 196  
 |||||||  
 QY 121 GGVFQLEKGRLSAEINRPDYLDFAESGQVYFGIALL 157  
 |||||||  
 DB 197 GGVFQLEKGRLSAEINRPDYLDFAESGQVYFGIALL 233

## RESULT 3

TNFA\_MACMU STANDARD; PRT; 233 AA.

AC P48094;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Cachectin).  
 GN TNF OR TNFA.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=96003435; PubMed=7561102;  
 RA Villinger F.J., Brar S.S., Mayne A.E., Chikala N., Ansari A.A.;  
 RT "Comparative sequence analysis of cytokine genes from human and  
 RT nonhuman primates.";  
 RL J. Immunol. 155:3946-3954(1995).

CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES. IT IS A CYTOKINE  
 CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF  
 CC CERTAIN TUMOR CELL LINES. IT IS IMPLICATED IN THE INDUCTION OF  
 CC CACHEXIA. IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION  
 CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION. IT CAN STIMULATE  
 CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN  
 CC CONDITIONS.  
 CC -1- SUBUNIT: HOMOTRIMER.  
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
 CC EXTRACELLULAR SOLUBLE FORM.  
 CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY  
 CC PROTEOLYTIC PROCESSING.  
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
 CC AND MALNUTRITION.

CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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 CC -----

DR EMBL: U19850; AAA86712.1; -.  
 DR HSSP: P01375; 4TSV.  
 DR InterPro: IPR003636; TNF\_abc.

DR InterPro: IPR000478; TNF\_family.  
DR Pfam: PF00229; TNF\_1.  
DR PRINTS: PR01234; TNECROSISFCR.  
DR ProDom: PD002012; TNF\_abc; 1.  
DR SMART: SM00207; TNF\_1.  
DR PROSITE: PS00251; TNF\_1; 1.  
DR Pfam: PF00229; TNF\_1.  
DR PROSITE: PS0049; TNF\_2; 1.  
KW Cytokine; Cytotoxin; Transmembrane; glycoprotein; signal-anchor.  
FT PROPEP 1 76  
FT CHAIN 77 233 TUMOR NECROSIS FACTOR.  
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
FT DISULFID 145 177 BY SIMILARITY.  
SQ SEQUENCE 233 AA; 25630 MW; 9F6F85050595FD59 CRC64;

Query Match 97.5%; Score 784; DB 1; Length 233;  
Best Local Similarity 97.5%; Pred. No. 5.2e-76;  
Matches 133; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 VRSSSRTPSDKPAHVAVANPQAEQQLQMLNRRANALLANGVELDNLVVPSEGLYLIYS 60  
DB 77 VRSSSRTPSDKPAHVAVANPQAEQQLQMLNRRANALLANGVELDNLVVPSEGLYLIYS 136  
QY 61 QVLFKGGCGSTHYVLTHTTSRIAVSYQTVNLSAISKPCQRTPGCAKAPKPEPIYL 120  
DB 137 QVLFKGGCGSTHYVLTHTTSRIAVSYQTVNLSAISKPCQRTPGCAKAPKPEPIYL 196  
QY 121 GGVFQLEKGDRLSAEINRPDYLDFAESGOVYFGIALL 157  
DB 197 GGVFQLEKGDRLSAEINRPDYLDFAESGOVYFGIALL 233

RESULT 4  
TNFA\_MACEFA STANDARD; PRT; 233 AA.  
AC P79337;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Tumor necrosis factor precursor (TNF-alpha) (Cachectin).  
GN TNF OR TNFA.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymphocytes;  
RA Tatsumi M.;  
RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES. IT IS A CYTOKINE  
WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF  
CERTAIN TUMOR CELL LINES. IT IS IMPLICATED IN THE INDUCTION OF  
CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION  
OR BY STIMULATION OF INTERLEUKIN 1 SECRETION. IT CAN STIMULATE  
CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN  
CONDITIONS.  
CC -1- SUBUNIT: HOMOTRIMER.  
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
EXTRACELLULAR SOLUBLE FORM.  
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY  
PROTEOLYTIC PROCESSING.  
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
AND MALNUTRITION.  
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
-----  
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CC -----  
DR EMBL: AB000513; BAA19131.1; -.  
DR HSSP: P01375; 4TSV.  
DR InterPro: IPR003636; TNF\_abc.  
DR InterPro: IPR000478; TNF\_family.  
DR Pfam: PF00229; TNF\_1.  
DR PRINTS: PR01234; TNECROSISFCR.  
DR ProDom: PD002012; TNF\_abc; 1.  
DR SMART: SM00207; TNF\_1.  
DR PROSITE: PS00251; TNF\_1; 1.  
DR Pfam: PF00229; TNF\_1.  
DR PROSITE: PS0049; TNF\_2; 1.  
KW Cytokine; Cytotoxin; Transmembrane; glycoprotein; signal-anchor.  
FT PROPEP 1 76  
FT CHAIN 77 233 TUMOR NECROSIS FACTOR.  
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
FT DISULFID 145 177 BY SIMILARITY.  
SQ SEQUENCE 233 AA; 25558 MW; 6ABF2C3AB132C217 CRC64;

Query Match 97.1%; Score 781; DB 1; Length 233;  
Best Local Similarity 96.8%; Pred. No. 1.1e-75;  
Matches 132; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VRSSSRTPSDKPAHVAVANPQAEQQLQMLNRRANALLANGVELDNLVVPSEGLYLIYS 60  
DB 77 VRSSSRTPSDKPAHVAVANPQAEQQLQMLNRRANALLANGVELDNLVVPSEGLYLIYS 136  
QY 61 QVLFKGGCGSTHYVLTHTTSRIAVSYQTVNLSAISKPCQRTPGCAKAPKPEPIYL 120  
DB 137 QVLFKGGCGSTHYVLTHTTSRIAVSYQTVNLSAISKPCQRTPGCAKAPKPEPIYL 196  
QY 121 GGVFQLEKGDRLSAEINRPDYLDFAESGOVYFGIALL 157  
DB 197 GGVFQLEKGDRLSAEINRPDYLDFAESGOVYFGIALL 233

RESULT 5  
TNFA\_PAPHU STANDARD; PRT; 233 AA.  
AC Q77510;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Tumor necrosis factor precursor (TNF-alpha) (Cachectin).  
GN TNF OR TNFA.  
OS Papio hamadryas ursinus (Chacma baboon).  
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoinae; Papio.  
OX NCBI\_TaxID=36229;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98147379; PubMed=9488055;  
RA Haudek S.B., Redl H., Schlag G., Glatz B.P.;  
RT "Complementary DNA (cDNA) sequence of baboon tumor necrosis factor  
alpha.";  
RT Mol. Immunol. 34:1041-1042(1997).  
CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES. IT IS A CYTOKINE  
WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF  
CERTAIN TUMOR CELL LINES. IT IS IMPLICATED IN THE INDUCTION OF  
CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION  
OR BY STIMULATION OF INTERLEUKIN 1 SECRETION. IT CAN STIMULATE  
CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN  
CONDITIONS.  
CC -1- SUBUNIT: HOMOTRIMER.  
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
EXTRACELLULAR SOLUBLE FORM.  
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY  
PROTEOLYTIC PROCESSING.  
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH



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CC      AND MALNUTRITION.
CC      -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF019633; AAC31675.1; -.
DR      HSSP; P01375; AFSV.
DR      InterPro: IPR003636; TNF_abc.
DR      InterPro: IPR000478; TNF_family.
DR      Pfam; PF00229; TNF; 1.
DR      PRINTS; PR01234; TNECROSISFCT.
DR      PRODOM; PD002012; TNF_abc; 1.
DR      SMART; SM00207; TNF_1; 1.
DR      PROSITE; PS00251; TNF_1; 1.
DR      PROSITE; PS50049; TNF_2; 1.
KW      Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
FT      PROPEP 1 76
FT      CHAIN 77 233
FT      TRANSMEM 36 56
FT      DISULFID 145 177
FT      SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
SQ      SEQUENCE 233 AA; 25658 MW; B9403255058D4A03 CRC64;

Query Match          97.0%; Score 780; DB 1; Length 233;
Best Local Similarity 96.8%; Pred. No. 1.4e-75;
Matches 152; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 VRSSRTSPDKPVAVHANVPAQEGOLWLNRRANLLANGVELRDNLVPSGGLYLIYS 60
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 77 VRSSRTSPDKPVAVHANVPAQEGOLWLNRRANLLANGVELRDNLVPSGGLYLIYS 136
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 61 QVLFKGGCPSPTHVLLHTTISRIVSYOTKYNLSAISPQORETPEGAEPKWPTEPYL 120
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 137 QVLFKGGCPSPTHVLLHTTISRIVSYOTKYNLSAISPQORETPEGAEPKWPTEPYL 196
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 121 GGVFQLEKGRDLSAEINRPDYLDFAESGQVYFGIALL 157
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 197 GGVFQLEKGRDLSAEINRPDYLDFAESGQVYFGIALL 233
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 6
TNFA_CANFA STANDARD; PRT; 233 AA.
AC PS1742; Q28339;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (cachectin).
GN TNF OR TNFA.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Fiers W., Beernart M.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RP [2]
RP SEQUENCE FROM N.A.
RA Zucker K., Lu P., Fuller L., Asthana D., Esquenazi V., Miller J.;
RT "Cloning and expression of the cDNA for canine tumor necrosis
RT factor-alpha in E. coli."
RL Lymphokine Res. 13:191-196(1994).
RN [3]
RP SEQUENCE OF 74-205 FROM N.A.
RC STRAIN-BEAGLE; TISSUE=Blood;
RA Gilmore W.H., Carter S.D., Bennett M., Barnes A., Kelly D.F.;
```

```
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES. IT IS A CYTOKINE
CC      WITH A WIDE VARIETY OF FUNCTIONS. IT CAN CAUSE CYTOLYSIS OF
CC      CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC      CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC      OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC      CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC      CONDITIONS.
CC      -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC      EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC      -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC      PROTEOLYTIC PROCESSING (BY SIMILARITY).
CC      -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC      CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC      AND MALNUTRITION.
CC      -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; X94932; CA64403.1; -.
DR      EMBL; S74068; AAB32391.1; -.
DR      EMBL; Z70046; CAA93908.1; -.
DR      HSSP; P01375; AFSV.
DR      InterPro: IPR003636; TNF_abc.
DR      InterPro: IPR000478; TNF_family.
DR      Pfam; PF00229; TNF; 1.
DR      PRINTS; PR01234; TNECROSISFCT.
DR      PRODOM; PD002012; TNF_abc; 1.
DR      SMART; SM00207; TNF_1; 1.
DR      PROSITE; PS00251; TNF_1; 1.
DR      PROSITE; PS50049; TNF_2; 1.
KW      Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
FT      PROPEP 1 76
FT      CHAIN 77 233
FT      TRANSMEM 36 56
FT      DISULFID 145 177
FT      CONFLICT 59 60
FT      CONFLICT 66 66
FT      CONFLICT 74 74
FT      CONFLICT 111 111
FT      CONFLICT 116 116
FT      CONFLICT 134 135
SQ      SEQUENCE 233 AA; 25447 MW; 7B2588FBC8B25340 CRC64;

Query Match          94.7%; Score 761; DB 1; Length 233;
Best Local Similarity 93.0%; Pred. No. 1.4e-73;
Matches 146; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 VRSSRTSPDKPVAVHANVPAQEGOLWLNRRANLLANGVELRDNLVPSGGLYLIYS 60
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 77 VRSSRTSPDKPVAVHANVPAQEGOLWLNRRANLLANGVELRDNLVPSGGLYLIYS 136
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 61 QVLFKGGCPSPTHVLLHTTISRIVSYOTKYNLSAISPQORETPEGAEPKWPTEPYL 120
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 137 QVLFKGGCPSPTHVLLHTTISRIVSYOTKYNLSAISPQORETPEGAEPKWPTEPYL 196
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 121 GGVFQLEKGRDLSAEINRPDYLDFAESGQVYFGIALL 157
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 197 GGVFQLEKGRDLSAEINRPDYLDFAESGQVYFGIALL 233
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 7
TNFA_FELCA STANDARD; PRT; 233 AA.
AC P19101;
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DT	01-NOV-1990 (Rel. 16, Created)
DT	01-NOV-1990 (Rel. 16, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	Tumor necrosis factor precursor (TNF-alpha) (Cachectin).
GN	TNF OR TNFA.
OC	Felis silvestris catus (Cat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX	NCBI_TaxId:9685;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Blood;
RA	MEDLINE=91016860; PubMed=2216740;
RT	McGraw R.A., Coffee B.W., Otto C.M., Drews R.T., Rawlings C.A.;
RL	"Gene sequence of feline tumor necrosis factor alpha.";
RN	Nucleic Acids Res. 18:5563-5563(1990).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Bone marrow;
RA	Daniel S.L., Brenner C.A., Legendre A.M., Solomon A., Rouse B.T.;
RL	Submitted (XXX-1993) to the EMBL/Genbank/DBJ databases.
CC	-1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE WITH A WIDE VARIETY OF FUNCTIONS. IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN CONDITIONS.
CC	-1- SUBUNIT: HOMOTRIMER.
CC	-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM.
CC	-1- PMW: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTEOLYTIC PROCESSING.
CC	-1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH AND MALNUTRITION.
CC	-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC	-----
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CC	-----
DR	EMBL; X54000; CAA37948.1; -.
DR	EMBL; M92061; AAA30818.1; -.
DR	PIR; S11688; S11688.
DR	HSP; P01375; ATSV.
DR	InterPro; IPR003636; TNF_abc.
DR	InterPro; IPR000478; TNF_Family.
DR	Pfam; PF00229; TNF; 1.
DR	PRINTS; PR01234; TNCRSISRCT.
DR	ProDom; PD002012; TNF_abc; 1.
DR	SMART; SM00207; TNF; 1.
DR	PROSITE; PS00251; TNF_2; 1.
DR	PROSITE; PS50049; TNF_2; 1.
FM	Cyclohex; Cyclohexin; Transmembrane; Glycoprotein; Signal-anchor. PROPEP
FT	CHAIN 1 76
FT	TRANSMEM 77 233
FT	DISULFID 36 56
FT	CONFLICT 145 177
FT	CONFLICT 28 28
FT	CONFLICT 104 104
FT	CONFLICT 151 151
FT	CONFLICT 155 155
FT	CONFLICT 210 210
FT	SEQUENCE 233 AA; 25322 MW; 434D339567862506 CRC64;
Query Match	90.5%; Score 728; DB 1; Length 233;
Best Local Similarity	91.1%; Pred. No. 4.6e-70;

	Matches	143	Conservative	4;	Mismatches	10;	Indels	0;	Gaps	0;
Oy	1	VRSSRSTSDKRPVAVVANPQAEQOLWLNRRANLLNGVLRLNQLVPSEGLYLITS	60	:						
Dd	77	LRSSTRSPSDEKRVAAHVANNPEAEGGLOLRSSRNALLANGVELTNOUKVPSDGLLITS	136	:						
Oy	61	OVLFQGQCSPSHVLTJTISRIVASYOTKVLLSAIKSPCOREPPEGAKPMKEPIYL	120	:						
Dd	137	OYLFFGGCCPSHVTTLTAISRFANSYTOKVVLLSAIKSPCOREPPEGAKPMKEPIYL	196	:						
Oy	121	GGVFLEKGDRLSAEINRPDYLDFAESGVFFGIATL	157	:						
Dd	197	GGVFLEKGDRISTEINTPAYIDFASGVGYFIATL	233	:						
RESULT	8	TNFA_HORSE		PRT; 234 AA.						
ID	TNFA_HORSE	STANDARD;	PRT; 234 AA.							
AC	P29553:									
DT	01-APR-1993 (Rel. 25, Created)									
DT	01-APR-1993 (Rel. 25, Last sequence update)									
DT	15-JUL-1999 (Rel. 38, last annotation update)									
De	Tumor necrosis factor precursor (TNF-alpha) (cachectin).									
Cn	TNF OR TNFA.									
OS	Equis caballus (Horse).									
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
RX	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.									
Nx	NCBI_Taxid=9796;									
Rn	[1]									
Rp	SEQUENCE FROM N.A.									
Rf	MEDLINE=92084125; PubMed=1748301;									
Rt	Su X., Morris D.D., McGraw R.A.;									
Rl	"Cloning and characterization of gene TNF alpha encoding equine tumor									
CC	necrosis factor alpha.";									
CC	Gene 107.319-321(1991)."									
CC	-I- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES. IT IS A CYTOKINE									
CC	WITH A WIDE VARIETY OF FUNCTIONS. IT CAN CAUSE CYTOLYSIS OF									
CC	CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF									
CC	CACHECTIA. IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION									
CC	OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE									
CC	CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN									
CC	CONDITIONS.									
CC	-I- SUBUNIT: HOMOTRIMER.									
CC	-I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN									
CC	EXTRACELLULAR SOLUBLE FORM.									
CC	-I- PFM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY									
CC	PROTEOLYTIC PROCESSING.									
CC	-I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.									
CC	-----									
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CC	or send an email to license@isb-sib.ch).									
CC	EMBL; M64087; AAA30959.1; .-									
Dr	PIR: J01344; J01344.									
Dr	HSSP: P01375; ATSV.									
Dr	InterPro: IPR000636; TNF_Abc.									
Dr	Interpro: IPRO00478; TNF_Family.									
Dr	Pfam: PF00229; TNF_1.									
Dr	PRINTS: PR01234; TECROSISFC.									
Dr	Prodont: PD002012; TNF_Abc; 1.									
Dr	SMART: SMD0207; TNF_1.									
Dr	PROSITE: PS00251; TNF_1; 1.									
Dr	PROSITE: PSS00049; TNF_2; 1.									
Kw	Cytokine; Cytotoxin; Transmembrane; Glycoprotein; signal-anchor.					</				

SEQUENCE	234 AA:	25469 MM:	E/79ACE91143DE373 CAC64:
Query Match	89.6%;	Score 720;	DB 1; Length 234;
Best Local Similarity	88.5%;	Pred. No. 3,3e-69;	
Matches 139;	Conservative 10;	Mismatches 8;	Indels 0; Gaps 0;
QY	1 VRSSRRPDSKPVAVHVNPAQEGQLMRRANALLANGVELRDNLVWPSSEGLYLITS 60		
DB	78 LRSSRRPDSKPVAVHVNPAQEGQLMRRANALLANGVELRDNLVWPSSEGLYLITS 137		
QY	61 QVLFPGQCCPSHYVLLTITISRIANSYOTKYNLLSAISPCQRETPEGAEAKPMKEPIYL 120		
DB	138 QVLFPGQCCPSHYVLLTITISRIANSYOTKYNLLSAISPCQRETPEGAEAKPMKEPIYL 197		
QY	121 GGVFLEKGRDLRAEINRPYLDFAESQGVYFGIATL 157		
DB	198 GGVFLEKGRDQLSAEINQPNYLDFAESQGVYFGIATL 234		
RESULT 9			
TNFA_PIG	STANDARD;	PRT;	232 AA.
ID AC	P23563;		
DT	01-NOV-1991 (Rel. 20, Created)		
DT	01-NOV-1991 (Rel. 20, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	Tumor necrosis factor precursor (TNF-alpha) (cachectin).		
GN	TNF OR TNFA.		
OS	Sus scrofa (Pig).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
OX	NCBI_TaxID:9823;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE-91016861; Pubmed-2216741;		
RA	Drews R.T., Coffee B.W., Prestwood A.K., McGraw R.A.;		
RT	"Gene sequence of porcine tumor necrosis factor alpha.;"		
RL	Nucleic Acids Res. 18:5564-5564(1990).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-Liver:		
RX	MEDLINE-91340150; Pubmed-1874444;		
RA	Kuhnert P., Wuehrlich C., Peterhans E., Pauli U.;		
RT	"The porcine tumor necrosis factor-encoding genes: sequence and		
RT	comparative analysis.;"		
RL	Gene 102:171-178(1991).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-Macrophage;		
RA	Choi C.S., Mollitor T.W., Lin G.F., Murtaugh M.P.;		
RT	"Complete nucleotide sequence of a cDNA encoding porcine tumor		
RT	necrosis factor-alpha.;"		
RL	Anin. Biotechnol. 2:97-105(1991).		
RN	[4]		
RP	SEQUENCE OF 44-232 FROM N.A.		
RX	MEDLINE-90034181; Pubmed-2478420;		
RA	Pauli U., Beutler B., Peterhans E.;		
RT	"Porcine tumor necrosis factor alpha: cloning with the polymerase		
RT	chain reaction and determination of the nucleotide sequence.;"		
RL	Gene 81:185-191(1989).		
CC	-1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE		
CC	WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF		
CC	CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF		
CC	CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION		
CC	OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE		
CC	CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN		
CC	CONDITIONS.		
CC	-1- SUBUNIT: HOMOTRIMER.		
CC	-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN		
CC	EXTRACELLULAR SOLUBLE FORM.		
CC	-1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY		
CC	PROTEOLYTIC PROCESSING.		

```

RP SEQUENCE FROM N.A.
RC STAIN-DUNKIN-HARTLEY;
RX MEDLINE-97462215; PubMed-9316485;
RA White A.W., Ioshimura T., Smith A.W., Westwick J., Watson M.L.;
RT "Always inflammation induced by recombinant guinea pig tumor necrosis
   factor-alpha.";
RL Am. J. Physiol. 273:L524-L530(1997).
CC -1 FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -1 SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1 SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -1 PM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING (BY SIMILARITY).
CC -1 DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1 SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
-----
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-----
DR EMBL, U39839; AAB06492.1; -.
DR EMBL, U77036; AAB19210.1; -.
DR HSSP: P06804; 2TNF.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF; 1.
DR PRINTS: PR01234; TNECROSISFCT.
DR PRODOM: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF; 1; 1.
DR PROSITE: PS00049; TNF; 2; 1.
KW Cytokine; Cytoctoxin; Transmembrane; Glycoprotein; Signal-anchor.
FT PROPEP      1
FT CHAIN       1
FT TRANSMEM    80      234      TUMOR NECROSIS FACTOR.
FT DISULFD     36      56      SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT FT         147      178      BY SIMILARITY.
SQ SEQUENCE    234 AA; 25793 MW; 7272C940393E7E9B CRC64;

Query Match          82.2%; Score 660.5; DB 1; Length 234;
Best Local Similarity 79.6%; Pred. No. 7e-63;
Matches 125; Conservative 19; Mismatches 12; Indels 1; Gaps 1;

OY 1 VRSSRRTPSDKRVAVVAVNPQAEGLQWLNRRANLLANGVELRDNOIIVPSSEGIYLITS 60
DB 79 LRSAQNNDNRKVAVHVVANQAEEELQWLISKRANLLANGMGLSNOLAIVPSDGIYLITS 138
OY 61 QVLFRGAGCSPTRHYLVLTITTSIRIASYOTKNVLISAIRSCPCORETPPEGAKPMKEPIYL 120
DB 139 QVLFRGAGCSPS-YLLTLFTVSRLAIVSYPEKVNLLSAIRSPCKEKPEGAERKPWEPIYL 197
OY 121 GGVPOLKEGRDLRSALRNPDVIDPAESGVYFGITAL 157
DB 198 GGVPQLQKGDRLSLADEVNLPPQYLDFAFDASQIFYGVIAL 234

RESULT 11
ID TNFA_MOUSE STANDARD: PRT; 235 AA.
AC P06804; 062326;
DT 01-JAN-1988 (Rel. 06, Created)
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DF 01-MAR-1989 (Rel. 10, Last sequence update)  
DE 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Tumor necrosis factor precursor (TNF-alpha) (Cachectin).  
GN TNF OR TNFA.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10099;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88224564; PubMed=2836146;  
RA Shirai T., Shimizu N., Shiojiri S., Horiyuchi S., Ito H.;  
RI "Cloning and expression in Escherichia coli of the gene for mouse  
RT tumor necrosis factor.";  
RL DNA 7:193-201(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85298296; PubMed=3898078;  
RA Pennica D., Hayflick J.S., Briningman T.S., Palladino M.A.,  
RA Goeddel D.V.;  
RT "Cloning and expression in Escherichia coli of the cDNA for murine  
RT tumor necrosis factor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 82:6060-6064(1985).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86149365; PubMed=2419912;  
RA Caput D., Beutler B., Hartog K., Thayer R., Brown-Shmer S.,  
RA Cerami A.;  
RT "Identification of a common nucleotide sequence in the  
RT 3'-untranslated region of mRNA molecules specifying inflammatory  
RT mediators.";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:1670-1674(1986).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85242112; PubMed=2989794;  
RA Fransen L., Mueller R., Marmenout A., Tavernier J., van der Heyden J.,  
RA Kawashima E., Cholliet A., Tizard R., van Heuverswyn H., van Vliet A.,  
RA Ruysschaert M.-R., Fiers W.;  
RT "Molecular cloning of mouse tumour necrosis factor cDNA and its  
RT eukaryotic expression.";  
RL Nucleic Acids Res. 13:4417-4429(1985).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87298639; PubMed=3040015;  
RA Shakhov A.N., Nedospasov S.A.;  
RT "Molecular cloning of genes coding for tumor necrosis factor.  
RT Complete nucleotide sequence of the genome copy of TNF-alpha in  
RT mice.";  
RL Bioorg. Khim. 13:701-705(1987).  
RN [6]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88067722; PubMed=3684584;  
RA Semon D., Kawashima E., Jongeneel C.V., Shakhov A.N., Nedospasov S.A.,  
RA "Nucleotide sequence of the murine TNF locus, including the TNF-alpha  
RT (tumor necrosis factor) and TNF-beta (lymphotoxin) genes.";  
RL Nucleic Acids Res. 15:9083-9084(1987).  
RN [7]  
RP SEQUENCE FROM N.A.  
RP STRAIN=CTS, AND NOD;  
RX MEDLINE=96013654; PubMed=7560085;  
RA Ikegami H., Makino S., Yamato E., Kawaguchi Y., Ueda H., Sakamoto T.,  
RA Takekawa K., Oghihara T.;  
RT "Identification of a new susceptibility locus for insulin-dependent  
RT diabetes mellitus by ancestral haplotype congenic mapping.";  
RL J. Clin. Invest. 96:1936-1942(1995).  
RN [8]  
RP SEQUENCE OF 80-99.  
RX MEDLINE=91097531; PubMed=2268312;  
RA Sherry B., Juc D.-W., Zentella A., Cerami A.;  
RT "Characterization of high molecular weight glycosylated forms of  
RT murine tumor necrosis factor.";  
RL Biochem. Biophys. Res. Commun. 173:1072-1078(1990).  
RN [9]



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DR EMBL: U14683; AAA50759.1; -.
DR HSSP: P01375; ATSV.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF; 1.
DR ProDom: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
DR Cytokine: Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
FM NON_TER .1
FT PROPEP <1 73
FT CHAIN 74 229
FT TRANSMEM 31 51
FT DISULFID 141 173
SQ SEQUENCE 229 AA; 24987 MW; 16DE5F7AA5A7DB35 CRC64;

Query Match 81.2%; Score 653; DB 1; Length 229;
Best Local Similarity 80.9%; Pred. No. 4.2e-62;
Matches 127; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

OY 1 VRSSRTSPDKPVAHVANVPAEQGLQWLNRRANLLANGVELRDNLVPSSEGLYLYS 60
DB 73 LRSSSQASINRPAHVAVNINAGQLMLDSCANALMANGVLENDQLVVPDGLYLYS 132
OY 61 QVLFPGGCPSTHVLLFTHTISRIAVSYOTKVNLSAIKSPCORETPEGAKEAKPMXEPYTL 120
DB 133 QVLFPGGCPSTPLPLFTHTISRIAVSYOTKVNLSAIKSPCHRETPENAEAKPMXEPYTL 192
OY 121 GGVFQLEKGRDLSAEINRPDYLDFAESGQVYFGIALL 157
DB 193 GGVFQLEKGRDLSAEINRPDYLDYVAESGQVYFGIALL 229

RESULT 13
TNFA_BOVIN STANDARD; PRT; 233 AA.
ID TNFA_BOVIN
AC Q06599; 018779;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Cachectin).
GN TNF OR TNFA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94083525; Pubmed=8260599;
RA Cludis I., Cleuter Y., Kettmann R., Buny A., Droogmans L.;
RT "Cloning and characterization of the tandemly arranged bovine
RT lymphocytin and tumor necrosis factor-alpha genes.";
RT Cytokine 5:336-341(1993).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=BOVAN, AND N'DAMA;
RA Itaghi F.;
RT "Bovine TNF-alpha gene.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 50-233 FROM N.A.
RC TISSUE=Blood;
RA MEDLINE=96006582; Pubmed=7590981;
RA Mettens B.E.L.C., Muriuki M., Gaidulis L.;
RT "Cloning of two members of the TNF-superfamily in cattle: CD40 ligand
RT and tumor necrosis factor alpha.";
RT Immunogenetics 42:430-431(1995).
CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES. IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS. IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF

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CC CACHEXIA. IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION. IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -1- SUBUNIT: HOMOTRIMER. TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -1- PM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
-----
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL: Z14137; CAA78511.1; -.
DR EMBL: AF011926; AAB84086.1; -.
DR EMBL: AF011927; AAB84087.1; -.
DR EMBL: Z48808; CAA8743.1; -.
DR PIR: S24642; S24642.
DR HSSP: P01375; ATSV.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF; 1.
DR PRINTS: PR01234; TNECROSISFCT.
DR ProDom: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
DR Cytokine: Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor;
KW Polymorphism.
FT PROPEP 1 77
FT CHAIN 78 233
FT TRANSMEM 36 56
FT DISULFID 145 177
FT VARIANT 48 48 F -> C (IN STRAIN N'DAMA).
FT CONFLICT 62 62 E -> EQ (IN REF. 3).
SQ SEQUENCE 233 AA; 25439 MW; 8AF55C02A9763B0 CRC64;

Query Match 81.1%; Score 652; DB 1; Length 233;
Best Local Similarity 80.3%; Pred. No. 5.5e-62;
Matches 126; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

OY 1 VRSSRTSPDKPVAHVANVPAEQGLQWLNRRANLLANGVELRDNLVPSSEGLYLYS 60
DB 77 LRSSSQASINRPAHVAVNINAGQLRMWDYSANALMANGVLENDQLVVPDGLYLYS 136
OY 61 QVLFPGGCPSTHVLLFTHTISRIAVSYOTKVNLSAIKSPCORETPEGAKEAKPMXEPYTL 120
DB 137 QVLFPGGCPSTPLPLFTHTISRIAVSYOTKVNLSAIKSPCHRETPENAEAKPMXEPYTL 196
OY 121 GGVFQLEKGRDLSAEINRPDYLDFAESGQVYFGIALL 157
DB 197 GGVFQLEKGRDLSAEINRPDYLDYVAESGQVYFGIALL 233

RESULT 14
TNFA_PERLE STANDARD; PRT; 235 AA.
ID TNFA_PERLE
AC P36939;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Cachectin).
GN TNF OR TNFA.

```

OS Peromyscus leucopus (White-footed mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Sigmodontinae;  
 CC Peromyscus.  
 CC NCBL\_TaxID=10041;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92218012; PubMed=1348497;  
 RA Crew M.D., Filipowsky M.E.;  
 RT \*Sequence of the tumor necrosis factor/cachectin (TNF) gene from  
 RT Peromyscus leucopus (family Cricetidae).";  
 RL Immunogenetics 35:351-353(1992).  
 CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE  
 CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF  
 CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF  
 CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION  
 CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE  
 CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN  
 CC CONDITIONS.  
 CC -1- SUBUNIT: HOMOTRIMER.  
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
 CC EXTRACELLULAR SOLUBLE FORM.  
 CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY  
 CC PROTEOLYTIC PROCESSING.  
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
 CC AND MALNUTRITION.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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 CC -----  
 CC DR EMBL: M59233; AAA40596.1; -  
 CC DR HSSP: P06804; 2TNF.  
 CC DR InterPro: IPR003636; TNF\_abc.  
 CC DR InterPro: IPR000478; TNF\_family.  
 CC DR Pfam: PF00229; TNF; 1.  
 CC DR PRINTS: PRO1234; TNECROSISFCT.  
 CC DR PRODOM: PD002012; TNF\_abc; 1.  
 CC DR SMART: SM00207; TNF; 1.  
 CC DR PROSITE: PS00251; TNF\_1; 1.  
 CC DR PROSITE: PS50049; TNF\_2; 1.  
 CC DR PROSITE: PS50049; TNF\_2; 1.  
 CC KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.  
 CC FT PROPEP 1 79 BY SIMILARITY.  
 CC FT CHAIN 80 235 TUMOR NECROSIS FACTOR.  
 CC FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
 CC FT DISULFID 148 179 BY SIMILARITY.  
 CC FT CARBOHD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC SQ SEQUENCE 235 AA; 25822 MW; 235A5CF9C9F9AC624 CRC64;  
 Query Match 81.0%; Score 651.5; DB 1; Length 235;  
 Best Local Similarity 78.3%; Pred.No.6.3e-62;  
 Matches 123; Conservative 20; Mismatches 13; Indels 1; Gaps 1;  
 QY 1 VSSSRTPSDKFAVAVPAQAGOLQWLRANALLANGVELRDQNLVPSGGLYIS 60  
 DB 80 LSSSSGNSDKFAVAVPAQAGOLQWLRANALLANGVELRDQNLVPSGGLYIS 139  
 QY 61 QVLFGQGPCSTHVLTLTISRAVSYQTKVNLISAIKSPCQRETPEGAEAKWKEPIYL 120  
 DB 140 QVLFGQGPCSTHVLTLTISRAVSYQTKVNLISAIKSPCQRETPEGAEAKWKEPIYL 198  
 QY 121 GGVFQLEKGDRLSAEINRPDYLDFAESGGVYFGIIL 157  
 DB 199 GGVFQLEKGDRLSAEINRPDYLDFAESGGVYFGIIL 235

RESULT 15  
 ID TNFA\_SHEEP STANDARD: PRT; 234 AA.  
 AC P23383;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Cachectin).  
 GN TNF OR TNFA.  
 OS Ovis aries (Sheep).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovidae; Caprinae; Ovis.  
 CC NCBL\_TaxID=9940;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=91067496; PubMed=2251151;  
 RA Young A.J., Hay J.B., Chan J.Y.C.;  
 RT \*Primary structure of ovine tumor necrosis factor alpha cDNA.";  
 RL Nucleic Acids Res. 18:6723-6723(1990).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Alveolar macrophage;  
 RX MEDLINE=92112044; PubMed=1765267;  
 RA Green I.R., Sargan D.R.;  
 RT \*Sequence of the cDNA encoding ovine tumor necrosis factor-alpha:  
 RT problems with cloning by inverse PCR.";  
 RL Gene 109:203-210(1991).  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92155784; PubMed=1786996;  
 RA Andrews A.E., Nash A.D., Batcham G.J., Brandon M.R.;  
 RT \*Molecular cloning, expression and characterization of ovine TNF  
 RT alpha.";  
 RL Immunol. Cell Biol. 69:273-283(1991).  
 CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE  
 CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF  
 CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF  
 CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION  
 CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE  
 CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN  
 CC CONDITIONS.  
 CC -1- SUBUNIT: HOMOTRIMER.  
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
 CC EXTRACELLULAR SOLUBLE FORM.  
 CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY  
 CC PROTEOLYTIC PROCESSING.  
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
 CC AND MALNUTRITION.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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 CC -----  
 CC DR EMBL: X55966; CAA39437.1; -  
 CC DR EMBL: X55152; CAA38952.1; -  
 CC DR EMBL: X56756; CAA40076.1; -  
 CC DR EMBL: A19163; CAA01445.1; -  
 CC DR PIR: S13114; S13114.  
 CC DR PIR: S20661; S20661.  
 CC DR PIR: JH0529; JH0529.  
 CC DR HSSP: P01375; 4TSV.  
 CC DR InterPro: IPR003636; TNF\_abc.  
 CC DR InterPro: IPR000478; TNF\_family.  
 CC DR Pfam: PF00229; TNF; 1.  
 CC DR PRINTS: PRO1234; TNECROSISFCT.

ProdOm: PD002012; TNF\_abc; 1.  
DR SMART; SM00207; TNF\_1; 1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.  
FT PROPEP 1 77  
FT CHAIN 78 234 TUMOR NECROSIS FACTOR.  
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
FT DISULFID 146 178 BY SIMILARITY.  
FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 63 63 MISSING (IN REF. 1).  
SQ SEQUENCE 234 AA; 25536 MM; 4BCF8CCAB7956B88 CRC64;

Query Match 80.8%; Score 650; DB 1; Length 234;  
Best Local Similarity 80.3%; Pred. No. 9.1e-62;  
Matches 126; Conservative 15; Mismatches 16; Indels 0; Gaps 0;  
Qy 1 VRSSRTPSDKPVAVHVNANPOAEGOLWLNRRANALLANGVELRDNOQVVPSEGLYLITS 60  
Db 78 LRSSQASNNKPVAVHVNANISAPQLRMGDSYANALMANGVELKDNQVLPIDGLILITS 137  
Qy 61 QVLFKGGCPSSTHVLTLHTISRIAVSYQTKVNLISAIKSPCQRETPEGAEAKPMXEPITL 120  
Db 138 QVLFKGGCPSSTHVLTLHTISRIAVSYQTKVNLISAIKSPCHRETLGAEAKPMYEPITQ 197  
Qy 121 GGVFQLEKGDRLSAFINRPDIYDFAESGVYFGITAL 157  
Db 198 GGVFQLEKGDRLSAFINRPDIYDFAESGVYFGITAL 234

Search completed: August 30, 2002, 17:37:50  
Job time: 97 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 30, 2002, 17:35:03 ; Search time 27.75 Seconds

(without alignments)  
978.746 Million cell updates/sec

Title: US-09-981-289a-20

Perfect score: 804

Sequence: 1 VRSSRTSPDKPAHVAVNP.....RPDYLDPAESGQVYFGIIAL 157

Scoring table: BIOSUM62

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL\_19:\*

- 1: sp.archaea:\*
- 2: sp.bacteria:\*
- 3: sp.fungi:\*
- 4: sp.human:\*
- 5: sp.invertebrate:\*
- 6: sp.mammal:\*
- 7: sp.mnc:\*
- 8: sp.organelle:\*
- 9: sp.phage:\*
- 10: sp.plant:\*
- 11: sp.todent:\*
- 12: sp.virus:\*
- 13: sp.vertebrate:\*
- 14: sp.unclassified:\*
- 15: sp.virus:\*
- 16: sp.bacteriap:\*
- 17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	797	99.1	157	4	043647
2	793	98.6	232	4	09UIV3
3	767	95.4	149	6	097543
4	714	88.8	149	6	097538
5	714	88.8	149	6	097538
6	714	88.8	149	6	097538
7	710	88.3	217	6	09BEG1
8	701	87.2	234	6	09BEG1
9	682	84.8	233	6	09BEG1
10	668	83.1	217	6	09BEG1
11	662	82.3	234	6	09BEG1
12	661	82.2	138	6	09BEG1
13	659	82.0	191	6	09BEG1
14	651.5	81.0	232	11	035853
15	649	80.7	216	6	09BEG1
16	638.5	79.4	235	11	09J127

17	635.5	79.0	235	11	09J126	09J126 rattus norv
18	634.5	78.9	156	11	09J124	09J124 sigmodon hl
19	620.5	77.2	216	6	09BEC9	09BEC9 ochotona pr
20	614	76.4	215	6	09BEE8	09BEE8 erinaceus e
21	608.5	75.7	217	11	09ERC6	09ERC6 peromyscus
22	607	75.5	217	6	09BEC5	09BEC5 tenrec ecau
23	604.5	75.2	216	11	070332	070332 mesocricetu
24	600	74.6	215	11	099ND1	099ND1 tamiasciuru
25	557	69.3	216	6	09BEE0	09BEE0 macropus ru
26	471.5	58.6	214	6	09BEE3	09BEE3 didelphis m
27	468	58.2	99	6	095LE8	095LE8 bos taurus
28	403	50.1	104	6	027978	027978 meriones un
29	299	37.2	101	11	09R136	09R136 canis fam11
30	293	36.4	65	6	095N81	095N81 canis fam11
31	292	36.3	66	4	09P102	09P102 homo sapien
32	271.5	33.8	205	11	09JMI2	09JMI2 marmota mon
33	271.5	33.8	205	11	09JMO9	09JMO9 marmota mon
34	237.5	29.5	225	13	09IB42	09IB42 paralichthy
35	235.5	29.3	225	13	09IB41	09IB41 paralichthy
36	220	27.4	246	13	09I970	09I970 oncorhynch
37	218.5	27.2	205	4	09UKS8	09UKS8 homo sapien
38	218	27.1	246	13	09I976	09I976 oncorhynch
39	216	26.9	127	11	09ERC9	09ERC9 mesocricetu
40	206	25.6	255	13	09I810	09I810 salvelinus
41	206	25.6	255	13	09DEP9	09DEP9 oncorhynch
42	197	24.5	41	6	09XT69	09XT69 canis fam11
43	182.5	22.7	174	4	09S150	09S150 homo sapien
44	171	21.3	280	6	09MYL6	09MYL6 macaca neme
45	171	21.3	280	6	09BDM5	09BDM5 macaca mula

#### ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	157	AA.
ID	043647				
AC	043647:				
DT	01-JUN-1998 (TREMBLrel. 06, Created)				
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)				
DE	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DT	TUMOR NECROSIS FACTOR ALPHA (FRAGMENT).				
GN	TNFA.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Jang J.S., Kim B.E.;				
RL	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.				
DR	EMBL: AF043342; AAC0542.1; ..				
DR	HSSP: P01375; IABM.				
DR	InterPro: IPR003636; TNF_abc.				
DR	InterPro: IPR000478; TNF_family.				
DR	Pfam: PF00229; TNF_1.				
DR	PRINTS: PR01234; TNFROSISFCT.				
DR	PRODom: PD002012; TNF_abc; 1.				
DR	SMART: SM00207; TNF_1.				
DR	PROSITE: PS00251; TNF_1; 1.				
DR	PROSITE: PS0049; TNF_2; 1.				
FT	NON_TER				
FT	1				
SO	SEQUENCE	157	AA:	17380	MM; D1344822267E9F20 CRC64;

Query Match 99.1%; Score 797; DB 4; Length 157;  
Best Local Similarity 98.7%; Pred. No. 2e-80;  
Matches 155; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VRSSRTSPDKPAHVAVNPQAEGQLQMLNRRANALLANGVELRDQQLVPPSEGLYLIS 60  
DB 1 VRSSRTSPDKPAHVAVNPQAEGQLQMLNRRANALLANGVELRDQQLVPPSEGLYLIS 60

QY 61 OVLFGGCGPSTHVLTHRTISRAVSYOTKVNLLSAIKSCPCOREPEGAANPWKEPIYL 120  
 DB 61 OVLFGGCGPSTHVLTHRTISRAVSYOTKVNLLSAIKSCPCOREPEGAANPWKEPIYL 120  
 QY 121 GGVFPLEKGDRLSAELNRPDIYDFAESGVYFGIITL 157  
 DB 121 GGVFPLEKGDRLSAELNRPDIYDFAESGVYFGIITL 157  
 RESULT 2  
 QYUIV3 PRELIMINARY: PRT: 232 AA.  
 AC QYUIV3:  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE TUMOR NECROSIS FACTOR.  
 GN TNF.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93272029; PubMed=8499947;  
 RA Irls F., Bougueleret L., Prieur S., Caterina D., Primas G., Perrot V.,  
 RA Juka J., Rodriguez-Tome P., Claverie J., Cohen D., Dausset J.;  
 RT "Dense Alu clustering and a potential new member of the NFkappa  
 RT family within a 90 kilobase HLA class III segment.";  
 RL Nat. Genet. 3:137-145(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96215741; PubMed=8629302;  
 RA Utans U., Oust W.C., McManus B.M., Wilson J.E., Arceci R.J.,  
 RA Holzinger I., de Baey A., Messer G., Kick G., Zwierzina H.,  
 RA Weiss E.H.;  
 RT "Cloning and genomic characterization of LST1: a new gene in the human  
 RT TNF region.";  
 RL Immunogenetics 42:315-322(1995).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93208881; PubMed=7916655;  
 RA Browning J.L., Ngam-ek A., Lawton P., Demarinis J., Tizard R.,  
 RA Chow E.P., Hession C., O'Brine-Greco B., Foley S.F., Ware C.F.;  
 RT "Lymphotoxin-beta: A new member of the TNF family that forms a  
 RT heteromeric complex with lymphotoxin on the cell surface.";  
 RL Cell 72:847-856(1993).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86016093; PubMed=2995927;  
 RA Nedwin G.E., Naylor S.L., Sakaguchi A.Y., Smith D., Jarrett-Nedwin J.,  
 RA Pennica D., Goeddel D.V., Gray P.W.;  
 RT "Human lymphotoxin and tumor necrosis factor genes: structure,  
 RT homology and chromosomal localization.";  
 RL Nucleic Acids Res. 13:6361-6373(1985).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9106846; PubMed=1670638;  
 RA Messer G., Spengler U., Jung M.C., Honold G., Bloemer K., Page G.R.,  
 RA Rietmuller G., Weiss E.H.;  
 RT "Polymorphic Structure of the Tumor Necrosis Factor (TNF) Locus: An  
 RT Ncol Polymorphism in the First Intron of the Human TNF-beta Gene  
 RT Correlates with A Variant Amino Acid in Position 26 and a Reduced  
 RT Level of TNF-beta Production.";  
 RL J. Exp. Med. 173:209-219(1991).  
 RN [7]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=91139175; PubMed=1671667;  
 RA Abraham L.J., Du D.C., Zahedi K., Dawkins R.L., Whitehead A.S.;  
 RT "Haplotypic polymorphisms of the TNFB gene.";  
 RL Immunogenetics 33:50-53(1991).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94362679; PubMed=8081366;  
 RA Albertella M.R., Campbell D.R.;  
 RT "Characterization of a novel gene in the human major  
 RT histocompatibility complex that encodes a potential new member of the  
 RT I kappa B family of proteins.";  
 RL Hum. Mol. Genet. 3:793-799(1994).  
 RN [9]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95324911; PubMed=7601445;  
 RA Peelman L., Chardon P., Nunes M., Renard C., Geoffroin C., Valman M.,  
 RA Van Zeveren A., Coppleters W., Van de Weghe A., Bouquet Y., Choy W.,  
 RA Strominger J., Spies T.;  
 RT "The BAT1 Gene in the MHC Encodes an Evolutionarily Conserved Putative  
 RT Nuclear RNA Helicase of the D-E-A-D Family.";  
 RL Genomics 26:210-218(1995).  
 RN [10]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20132445; PubMed=10668961;  
 RA Neville M.J., Campbell R.D.;  
 RT "Alternative splicing of the LST-1 gene located in the major  
 RT histocompatibility complex on human chromosome 6.";  
 RL DNA Seq. 8:155-160(1997).  
 RN [11]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98035883; PubMed=9367684;  
 RA de Baey A., Fellerhoff B., Maier S., Martinozzi S., Weidie U.,  
 RA Weiss E.H.;  
 RT "Complex expression pattern of the TNF region gene LST1 through  
 RT differential regulation, initiation, and alternative splicing.";  
 RL Genomics 45:591-600(1997).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98149985; PubMed=9480751;  
 RA Shina T., Tamiya G., Oka A., Yamagata T., Yamagata N., Kikkawa E.,  
 RA Goto K., Mizuki N., Watanabe K., Fukuzumi Y., Taguchi S., Sugawara C.,  
 RA Ono A., Chen L., Yamazaki M., Tashiro H., Ando A., Ikemura T.,  
 RA Kimura M., Inoko H.;  
 RT "Nucleotide sequencing analysis of the 146-kilobase segment around the  
 RT Ikb1 and MICA genes at the centromeric end of the HLA class I  
 RT region.";  
 RL Genomics 47:372-382(1998).  
 DR EMBL: Y14768; CAA75070.1; -;  
 DR HSSP: P01375; 4TSV.  
 DR InterPro: IPR003636; TNF\_abc.  
 DR InterPro: IPR000478; TNF\_family.  
 DR Pfam: PF00229; TNF; 1.  
 DR PRINTS: PR01234; TNFCROSISFCT.  
 DR PRODOM: PD002012; TNF\_abc; 1.  
 DR SMART: SM00207; TNF; 1.  
 DR PROSITE: PS00049; TNF\_1; 1.  
 DR PROSITE: PS00051; TNF\_2; 1.  
 SQ SEQUENCE 232 AA; 25446 MW; EAD71B19C6AE0D03 CRC64;

Query Match 98.6%; Score 793; DB 4; Length 232;  
 Best Local Similarity 99.4%; Pred. No. 9.3e-80;  
 Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SSSRPSDKPVAHVYVANOAGQQLQMLNRRANALLANGVELRDNLVVPSEGLYLIYSQV 62  
 DB 78 SSSRPSDKPVAHVYVANOAGQQLQMLNRRANALLANGVELRDNLVVPSEGLYLIYSQV 137  
 QY 63 LFKGGCGPSTHVLTHRTISRAVSYOTKVNLLSAIKSCPCOREPEGAANPWKEPIYIGG 122  
 DB 138 LFKGGCGPSTHVLTHRTISRAVSYOTKVNLLSAIKSCPCOREPEGAANPWKEPIYIGG 197

QY 123 VFQLEKGRSLSAEINRPDYLDFAESGQVYFGIIL 157  
|||||  
Db 198 VFQLEKGRSLSAEINRPDYLDFAESGQVYFGIIL 232

RESULT 3  
097543 PRELIMINARY: PRT: 149 AA.

AC 097543;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
DE TUMOR NECROSIS FACTOR ALPHA (FRAGMENT).  
GN TNF-ALPHA.  
OS Actus nancyanae (Owl monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Actus.  
OX NCBI\_TaxID=37293;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Echeverry S.J., Hernandez E., Moreno A., Patarroyo M.E., Murillo L.A.;  
RT "Identification, cloning and sequencing of different Interleukin genes  
in 4 Actus species."  
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF014513; AAD01539.1; -.  
DR HSSP; P01375; ATSV.  
DR InterPro; IPR003636; TNF\_abc.  
DR InterPro; IPR000478; TNF\_family.  
DR Pfam; PF00229; TNF; 1.  
DR PRINTS; PRO1234; TNECROSISFCT.  
DR PRODOM; PD002012; TNF\_abc; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
FT NON\_TER 1  
FT NON\_TER 149  
SQ SEQUENCE 149 AA; 16466 MW; 3C2A6140778EFABA CRC64;

Query Match 95.4%; Score 767; DB 6; Length 149;  
Best Local Similarity 99.3%; Pred. No. 3.9e-77;  
Matches 148; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 PSDKPVAVHANPQAEGLQWLNRRANLLANGVELRDNOQVPSGGLYLYSQVLFKQ 67  
|||||  
Db 1 PSDKPVAVHANPQAEGLQWLNRRANLLANGVELRDNOQVPSGGLYLYSQVLFKQ 60  
|||||  
QY 68 GCPSTHVLTHRTISRIAVSYQTKVNLISAISPCQRETPEGAEAKPWKEPTILGCVFQLE 127  
|||||  
Db 61 GCPSTHVLTHRTISRIAVSYQTKVNLISAISPCQRETPEGAEAKPWKEPTILGCVFQLE 120  
|||||  
QY 128 KGRSLSAEINRPDYLDFAESGQVYFGIIL 156  
|||||  
Db 121 KGRSLSAEINRPDYLDFAESGQVYFGIIL 149  
|||||  
RESULT 4  
097538 PRELIMINARY: PRT: 149 AA.

RT in 4 Actus species";  
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF014508; AAD01534.1; -.  
DR HSSP; P01375; ATSV.  
DR InterPro; IPR003636; TNF\_abc.  
DR InterPro; IPR000478; TNF\_family.  
DR Pfam; PF00229; TNF; 1.  
DR PRINTS; PRO1234; TNECROSISFCT.  
DR PRODOM; PD002012; TNF\_abc; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
FT NON\_TER 1  
FT NON\_TER 149  
SQ SEQUENCE 149 AA; 16415 MW; 86F1B9BCED16E689 CRC64;

Query Match 88.8%; Score 714; DB 6; Length 149;  
Best Local Similarity 91.9%; Pred. No. 3e-71;  
Matches 137; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 8 PSDKPVAVHANPQAEGLQWLNRRANLLANGVELRDNOQVPSGGLYLYSQVLFKQ 67  
|||||  
Db 1 PSDKPVAVHANPQAEGLQWLNRRANLLANGVELRDNOQVPSGGLYLYSQVLFKQ 60  
|||||  
QY 68 GCPSTHVLTHRTISRIAVSYQTKVNLISAISPCQRETPEGAEAKPWKEPTILGCVFQLE 127  
|||||  
Db 61 GCPSTHVLTHRTISRIAVSYQTKVNLISAISPCQRETPEGAEAKPWKEPTILGCVFQLE 120  
|||||  
QY 128 KGRSLSAEINRPDYLDFAESGQVYFGIIL 156  
|||||  
Db 121 KGRSLSAEINRPDYLDFAESGQVYFGIIL 149  
|||||  
RESULT 5  
097TG8 PRELIMINARY: PRT: 149 AA.

AC 097TG8;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE TUMOR NECROSIS FACTOR ALPHA (FRAGMENT).  
GN TNF-ALPHA.  
OS Actus nigricaps (black-headed night monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Actus.  
OX NCBI\_TaxID=57175;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Patarroyo M.E., Hernandez E., Echeverry S.J., Mendez J.A.,  
RT "Actus nigricaps gene for TNF alpha."  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF097328; AAF21303.1; -.  
DR HSSP; P01375; ATSV.  
DR InterPro; IPR003636; TNF\_abc.  
DR InterPro; IPR000478; TNF\_family.  
DR Pfam; PF00229; TNF; 1.  
DR PRINTS; PRO1234; TNECROSISFCT.  
DR PRODOM; PD002012; TNF\_abc; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
FT NON\_TER 1  
FT NON\_TER 149  
SQ SEQUENCE 149 AA; 16415 MW; 86F1B9BCED16E689 CRC64;

Query Match 88.8%; Score 714; DB 6; Length 149;  
Best Local Similarity 91.9%; Pred. No. 3e-71;  
Matches 137; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 8 PSDKPVAVHANPQAEGLQWLNRRANLLANGVELRDNOQVPSGGLYLYSQVLFKQ 67

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Db 1 PSDFPVAHVANPQAEQOLWLNRRANALLANGVELRDNDQLVVPSSEGLYLYSQVLFKRGQ 60
QY 68 GCPSTHVLTTHTISRIVSYQTKVNLISAIKSPQCRTPPEGAEPKXPPEPIYLGVPFLE 127
Db 61 GCPSTFMLTHTISRIVSAIVAKVNLISAIKSPQCRTPPEGAEPKXPPEPIYLGVPFLE 120
QY 128 KGDRLSAEINRPDYLDFAESGQVFGITA 156
Db 121 KGDRLSAEINRPDYLDFAESGQVFGITA 149

RESULT 6
Q9BEG0 PRELIMINARY; PRT; 217 AA.
ID Q9BEG0
AC Q9BEG0:
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE TUMOR NECROSIS FACTOR (FRAGMENT).
GN TNFA.
OS Cyclopes diactylus (silky anteater).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Myrmecophagidae; Cyclopes.
OX NCBI_TaxID=84074;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
RT their sister group."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286828; CAC28514.1; -.
DR HSSP; P01375; IABM.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF_1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF_1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 217 AA; 23753 MW; F760E887F6C29EBB CRC64;

Query Match 88.8%; Score 714; DB 6; Length 217;
Best Local Similarity 91.3%; Pred. No. 4.9e-71; Indels 0; Gaps 0;
Matches 136; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 VRSSRTPSDKPVAVVAVANPQAEQOLWLNRRANALLANGVELRDNDQLVVPSSEGLYLYIS 60
Db 69 LRSSSRTPSDKPVAVVAVANPQAEQOLWLSRRANALLANGVELRDNDQLVVPSDGLYLYIS 128
QY 61 QVLFKGGCPSSTHVLTTHTISRIVSYQTKVNLISAIKSPQCRTPPEGAEPKXPPEPIYL 120
Db 129 QVLFKGGCPSSTHVLTTHTISRIVSYQTKVNLISAIKSPQCRTPPEGAEPKXPPEPIYL 188
QY 121 GGVFQLEKGDRLSAEINRPDYLDFAESGQ 149
Db 189 GGVFQLEKGDRLSAEINRPDYLDFAESGQ 217

RESULT 7
Q9BEG1 PRELIMINARY; PRT; 217 AA.
ID Q9BEG1
AC Q9BEG1:
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE TUMOR NECROSIS FACTOR (FRAGMENT).
GN TNFA.
OS Bradypus tridactylus (Pale-throated three-toed sloth).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Bradypodidae; Bradypus.
OX NCBI_TaxID=9354;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
RT their sister group."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286827; CAC28513.1; -.
DR HSSP; P01375; IABM.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF_1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF_1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 217 AA; 23655 MW; A7056710B6238074 CRC64;

Query Match 88.3%; Score 710; DB 6; Length 217;
Best Local Similarity 91.3%; Pred. No. 1.4e-70; Indels 0; Gaps 0;
Matches 136; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 VRSSRTPSDKPVAVVAVANPQAEQOLWLNRRANALLANGVELRDNDQLVVPSSEGLYLYIS 60
Db 69 LRSSSRTPSDKPVAVVAVANPQAEQOLWLSRRANALLANGVELRDNDQLVVPSDGLYLYIS 128
QY 61 QVLFKGGCPSSTHVLTTHTISRIVSYQTKVNLISAIKSPQCRTPPEGAEPKXPPEPIYL 120
Db 129 QVLFKGGCPSSTHVLTTHTISRIVSYQTKVNLISAIKSPQCRTPPEGAEPKXPPEPIYL 188
QY 121 GGVFQLEKGDRLSAEINRPDYLDFAESGQ 149
Db 189 GGVFQLEKGDRLSAEINRPDYLDFAESGQ 217

RESULT 8
Q9TTJ3 PRELIMINARY; PRT; 234 AA.
ID Q9TTJ3
AC Q9TTJ3:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE TUMOR NECROSIS FACTOR-ALPHA.
GN TNFA.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=THOROUGHbred; TISSUE=ARTERIAL ENDOTHELIUM;
RA Ishida N., Sato F., Hasegawa T.;
RT "Molecular cloning of equine tumor necrosis factor-alpha mRNA.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB035735; BAA88349.1; -.
DR HSSP; P01375; IABM.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF_1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF_1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 234 AA; 25430 MW; 2384D4950A21F377 CRC64;

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Query Match      87.2%; Score 701; DB 6; Length 234;
Best Local Similarity 87.3%; Pred. No. 1.5e-69;
Matches 137; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

OY 1 VRSSRTSPDKPVAVVYVAVVPAQEGOLQWLNRRANALLANGVELNDQNVVPSGGLYLYIS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 78 LRSSRTSPDKPVAVVYVAVVPAQEGOLQWLSGRANALLANGVELNDQNVVPLDGLYLYIS 137
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

OY 61 QVLFKGGCSTHVLHTHTISRIYVSYOTKYNLSAISPQORETPEGAEKPMXEPIYL 120
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 138 QVLFKGGCSTHVLHTHTISRIYVSYPSKYNLSAISPQORETPEGAEKPMXEPIYL 197
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

OY 121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYEGIIAL 157
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 198 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYEGIIAL 234
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9
ID Q9BEA1 PRELIMINARY; PRT; 233 AA.
AC Q9BEA1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE TUMOR NECROSIS FACTOR ALPHA.
GN TNF-ALPHA.
OS Turstrops truncatus (Atlantic bottle-nosed dolphin).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Turstrops.
OX NCBI_TaxID=9739;
RN [1]
RP SEQUENCE FROM N.A.
RA Shoji Y., Inoue Y., Jinbo T., Itou T., Sakai T.;
RT "Molecular cloning and functional expression of Bottle-Nosed
   Dolphin(Turstrops truncatus) Tumor necrosis factor alpha.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049358; BAB39855.1; -.
DR HSSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF_1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF_1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 233 AA; 25404 MW; 71CC39C699CC49D9 CRC64;

Query Match      84.8%; Score 682; DB 6; Length 233;
Best Local Similarity 83.4%; Pred. No. 1.9e-67;
Matches 131; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

OY 1 VRSSRTSPDKPVAVVYVAVVPAQEGOLQWLNRRANALLANGVELNDQNVVPSGGLYLYIS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 77 LRSSRTSPDKPVAVVYVAVVPAQEGOLQWLNRRANALLANGVELNDQNVVPLDGLYLYIS 136
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

OY 61 QVLFKGGCSTHVLHTHTISRIYVSYOTKYNLSAISPQORETPEGAEKPMXEPIYL 120
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 137 QVLFKGGCSTHVLHTHTISRIYVSYPSKYNLSAISPQORETPEGAEKPMXEPIYL 196
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

OY 121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYEGIIAL 157
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 197 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYEGIIAL 233
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 10
ID Q9BEF4 PRELIMINARY; PRT; 217 AA.
AC Q9BEF4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

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DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TUMOR NECROSIS FACTOR (FRAGMENT).
GN TNFA.
OS Cabassous unicinctus (Southern naked-tailed armadillo).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Daelypodidae; Cabassous.
OX NCBI_TaxID=48852;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
   their sister group.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286829; CAC28518.1; -.
DR HSSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF_1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF_1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 217 AA; 23742 MW; 83C591DD6883FD86 CRC64;

Query Match      83.1%; Score 668; DB 6; Length 217;
Best Local Similarity 85.9%; Pred. No. 6.2e-66;
Matches 128; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

OY 1 VRSSRTSPDKPVAVVYVAVVPAQEGOLQWLNRRANALLANGVELNDQNVVPSGGLYLYIS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 69 LRSSRTSPDKPVAVVYVAVVPAQEGOLQWLNRRANALLANGVELNDQNVVPSGGLYLYIS 128
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

OY 61 QVLFKGGCSTHVLHTHTISRIYVSYOTKYNLSAISPQORETPEGAEKPMXEPIYL 120
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 129 QVLFKGGCSTHVLHTHTISRIYVSYPSKYNLSAISPQORETPEGAEKPMXEPIYL 188
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

OY 121 GGVFQLEKGDRLSAEINRPDYLDFAESQ 149
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 189 GGVFQLEKGDRLSAEINRPDYLDFAESQ 217
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
ID Q28320 PRELIMINARY; PRT; 234 AA.
AC Q28320;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE TNF-ALPHA.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA Takakura H., Mori Y., Tatsumi M.;
RT "Molecular cloning of caprine TNF-alpha cDNA and its expression in
   E.coli and insect cells.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; D86587; BAA13130.1; -.
DR HSSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF_1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF_1.
DR PROSITE; PS00251; TNF_1; 1.

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DR PROSITE: PS50049; TNF\_2; 1.  
SQ SEQUENCE 234 AA; 25519 MW; 9768E33BBAB041 CRC64;

Query Match 82.3%; Score 662; DB 6; Length 234;  
Best Local Similarity 81.5%; Pred. No. 3,2e-65;  
Matches 128; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 1 VRSSRTSPDKPAHVAVNPAQEQQLQWLNRRANALLANGVELRDNLVPSGGLYLYS 60  
DB 78 LRSSSQASSNKPAHVAVNANISAPGQLRMGDSYANALKANGVELKDNLVPTDGLYLYS 137  
QY 61 QVLFKGGCPSSTVLLTHTISRAVSQTKVNLISAIRSPCORETPEGAEAKPWEPITYL 120  
DB 138 QVLFKGGCPSSTVLLTHTISRAVSQTKVNLISAIRSPCHRETPEGAEAKPWEPITYQ 197  
QY 121 GGVFQLEKGRDLSAEINRPDYLDFAESQVYFGIIAL 157  
DB 198 GGVFQLEKGRDLSAEINRPDYLDFAESQVYFGIIAL 234

RESULT 12  
Q9TMG7 PRELIMINARY; PRT; 138 AA.  
AC Q9TMG7:  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
DE TUMOR NECROSIS FACTOR ALPHA (FRAGMENT).  
GN TNF-ALPHA.  
OS Aotus lemurinus (Northern gray-necked night monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.  
CX NCB1\_TaxID=43147;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,  
RA Pararoyo M.E.;  
RT "Aotus lemurinus gene for TNF alpha."  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF097329; AAF21304.1; -  
DR HSSP; P01375; 4TSV.  
DR InterPro: IPR003636; TNF\_abcd.  
DR InterPro: IPR000478; TNF\_family.  
DR Pfam: PF00229; TNF\_1.  
DR PRINTS; PR01234; TNECROSISFCT.  
DR PRODOM; PD002012; TNF\_abcd; 1.  
DR SMART; SM00207; TNF\_1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
FT NON\_TER 1  
SQ SEQUENCE 138 AA; 15269 MW; 29275EE4F4CD5068 CRC64;

Query Match 82.2%; Score 661; DB 6; Length 138;  
Best Local Similarity 92.0%; Pred. No. 2e-65;  
Matches 126; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 8 PSKRPVAVVAVNPAQEQQLQWLNRRANALLANGVELRDNLVPSGGLYLYS 67  
DB 1 PSKRPVAVVAVNPAQEQQLQWLNRRANALLANGVELRDNLVPSGGLYLYS 60  
QY 68 GCPSTHVLHTISRAVSQTKVNLISAIRSPCORETPEGAEAKPWEPITYL 127  
DB 61 GCPSTHVLHTISRAVSQTKVNLISAIRSPCORETPEGAEAKPWEPITYL 120  
QY 128 KGDRLSAEINRPDYLD 144  
DB 121 KGDRLSAEINRPDYLD 137

RESULT 13  
Q9MYZ2

ID Q9MYZ2 PRELIMINARY; PRT; 191 AA.

AC Q9MYZ2:  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE TUMOR NECROSIS FACTOR ALPHA (FRAGMENT).  
OS Capra hircus (Goat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprine; Capra.  
CX NCB1\_TaxID=9925;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA TISSUE-OVARIAN FOLLICLE;  
RA Wang B., Zhang Y.;  
RT "Goat ovarian TNF alpha cDNA sequence."  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF276985; AAF87741.1; -  
DR HSSP; P01375; 4TSV.  
DR InterPro: IPR003636; TNF\_abcd.  
DR InterPro: IPR000478; TNF\_family.  
DR Pfam; PF00229; TNF\_1.  
DR PRINTS; PR01234; TNECROSISFCT.  
DR PRODOM; PD002012; TNF\_abcd; 1.  
DR SMART; SM00207; TNF\_1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
FT NON\_TER 1  
SQ SEQUENCE 191 AA; 20889 MW; 4F887EAF4320CC96 CRC64;

Query Match 82.0%; Score 659; DB 6; Length 191;  
Best Local Similarity 81.5%; Pred. No. 5,2e-65;  
Matches 128; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 VRSSRTSPDKPAHVAVNPAQEQQLQWLNRRANALLANGVELRDNLVPSGGLYLYS 60  
DB 35 LRSSSQASSNKPAHVAVNANISAPGQLRMGDSYANALKANGVELKDNLVPTDGLYLYS 94  
QY 61 QVLFKGGCPSSTVLLTHTISRAVSQTKVNLISAIRSPCORETPEGAEAKPWEPITYL 120  
DB 95 QVLFKGGCPSSTVLLTHTISRAVSQTKVNLISAIRSPCHRETPEGAEAKPWEPITYQ 154  
QY 121 GGVFQLEKGRDLSAEINRPDYLDFAESQVYFGIIAL 157  
DB 155 GGVFQLEKGRDLSAEINRPDYLDFAESQVYFGIIAL 191

RESULT 14  
O35853 PRELIMINARY; PRT; 232 AA.  
AC O35853:  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
DE TUMOR NECROSIS FACTOR ALPHA.  
GN TNFA.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
CX NCB1\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN-A/J;  
RX MEDLINE=97246744; PubMed=9089109;  
RA Iradi F., Teale A.;  
RT "Cloning and sequencing of the tnfa genes of three inbred mouse strains."  
RL Immunogenetics 45:459-461(1997).  
DR EMBL; U68414; AAB65593.1; -  
DR HSSP; P06804; 2TNF.  
DR InterPro: IPR003636; TNF\_abcd.  
DR InterPro: IPR000478; TNF\_family.

DR Pfam: PF00229; TNF; 1.  
 DR PRINTS: PRO1234; TNECROSISFCT.  
 DR PRODOM: PD002012; TNF\_abc; 1.  
 DR SMART: SM00207; TNF; 1.  
 DR PROSITE: PS00251; TNF\_1; 1.  
 DR PROSITE: PS50049; TNF\_2; 1.  
 SQ SEQUENCE 232 AA; 25513 MW; 2ED6DA8EDDCAAD8 CRC64;

Query Match 81.0%; Score 651.5; DB 11; Length 232;  
 Best Local Similarity 78.7%; Pred. No. 4.6e-64;  
 Matches 122; Conservative 19; Mismatches 13; Indels 1; Gaps 1;

OY 3 SSSRTSPDKPVAVHVNPAQEGOLQWLNRRANALLANGVELRDNLVPSSEGLYLYSQV 62  
 DB 79 SSSQSSDPKPVAVHVNPAQEGOLQWLNRRANALLANGVELRDNLVPSSEGLYLYSQV 138  
 OY 63 LFKGGGCPSTHVLTHRTISRIAVSYQTKVNLISAIKSPCQRETPGAEAKPMXEPYILGG 122  
 DB 139 LFKGGGCPD-VYLLTHHTVSRFAISYQEKVNLISAVKSPCKPTPEGAEAKPMXEPYILGG 197  
 OY 123 VFQLEKGDRLSAEINRPDYLDFAESGQYFEGIAL 157  
 DB 198 VFQLEKGDQLSAEVLNPKYLDFAESGQYFEGIAL 232

## RESULT 15

O9BEC4  
 ID O9BEC4 PRELIMINARY; PRT; 216 AA.  
 AC O9BEC4;  
 DT 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE TUMOR NECROSIS FACTOR (FRAGMENT).  
 GN TNFA.  
 OS Talpa europaea (European mole).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Insectivora; Talpidae; Talpa.  
 OX NCBI\_TaxID=9373;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA van Dijk M.A.M., de Jong W.M.;  
 RT "Indels indicate that rodents are monophyletic and lagomorphs are  
 RT their sister group."  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ286831; CAC28539.1; -.  
 DR HSSP: P01375; 1A8M.  
 DR InterPro: IPR003636; TNF\_abc.  
 DR InterPro: IPR000478; TNF\_family.  
 DR Pfam: PF00229; TNF; 1.  
 DR PRINTS: PRO1234; TNECROSISFCT.  
 DR PRODOM: PD002012; TNF\_abc; 1.  
 DR SMART: SM00207; TNF; 1.  
 DR PROSITE: PS00251; TNF\_1; 1.  
 DR PROSITE: PS50049; TNF\_2; 1.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 FT 216  
 SQ SEQUENCE 216 AA; 23542 MW; FFEFE8DBBD27836 CRC64;

Query Match 80.7%; Score 649; DB 6; Length 216;  
 Best Local Similarity 84.6%; Pred. No. 7.9e-64;  
 Matches 126; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

OY 1 VSSSRTPSDKPVAVHVNPAQEGOLQWLNRRANALLANGVELRDNLVPSSEGLYLYS 60  
 DB 68 LSSSRTPGDKPVAVHVNPAQEGOLQWLNRRANALLANGVELTNNQLVPSDGLYLYS 127  
 OY 61 QVLFKGQGPCSTHVLTHRTISRIAVSYQTKVNLISAIKSPCQRETPGAEAKPMXEPYIL 120  
 DB 128 QVLFKGQGPCSNVLVLTHTIORTAVSYEDAVIDLSAIKSPCQRETPGAEAKPMXEPYIL 187  
 OY 121 GGVFQLEKGDRLSAEINRPDYLDFAESGQ 149

DB 188 GGVFQLEKGDRLSANINLPKYLDFAGQSQ 216

Search completed: August 30, 2002, 17:37:32  
 Job time: 149 sec

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